

09310667.051299

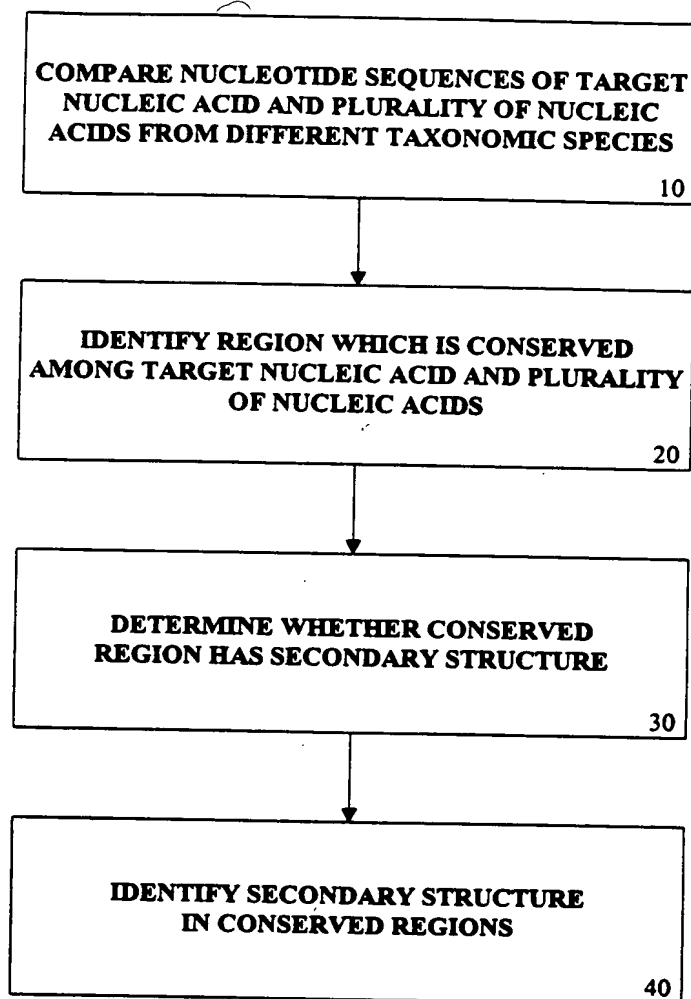


FIGURE 1

09310567.051299
662T50/990TE60

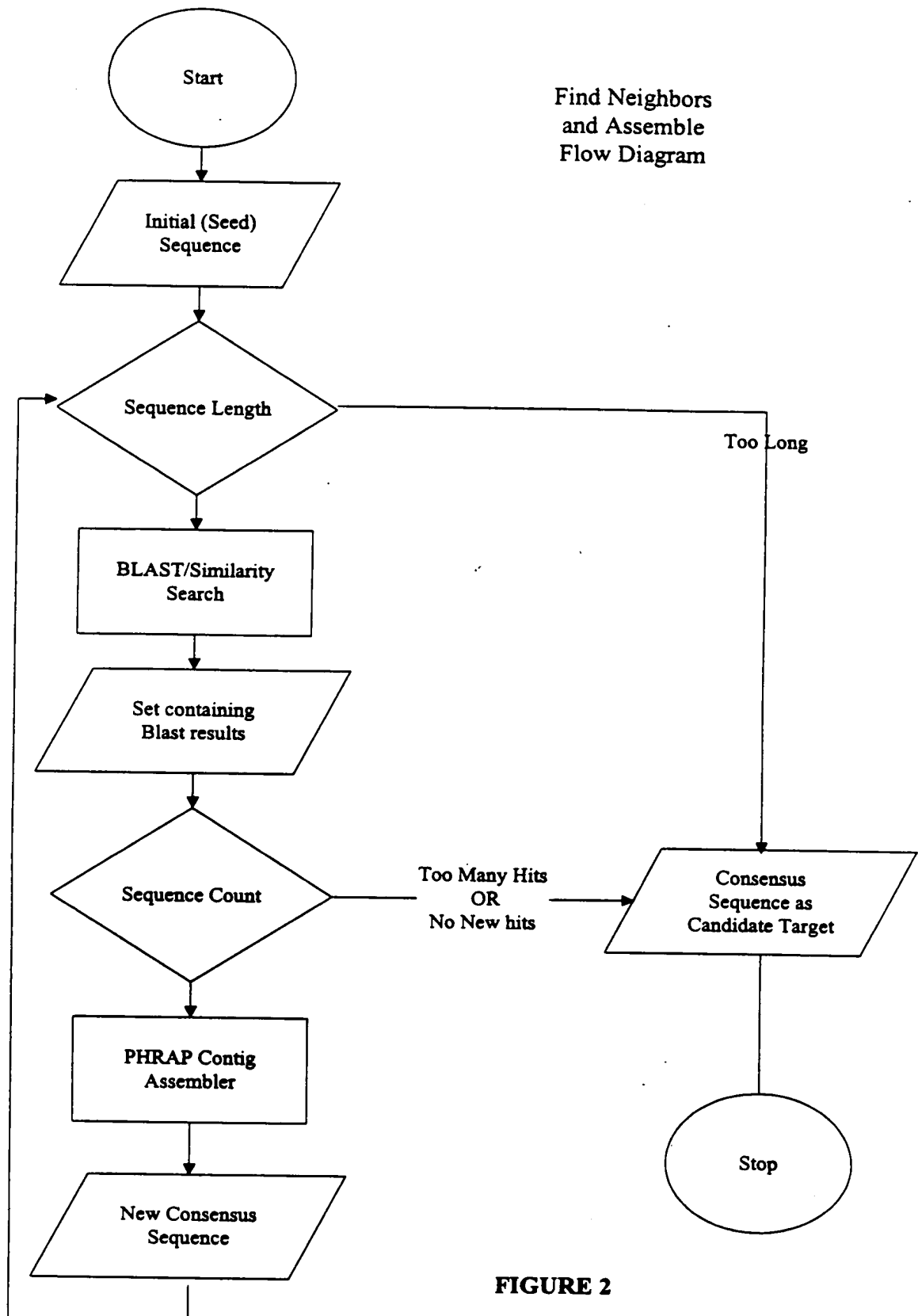


FIGURE 2

09310667.051299
1662T507990T660

BlastParse

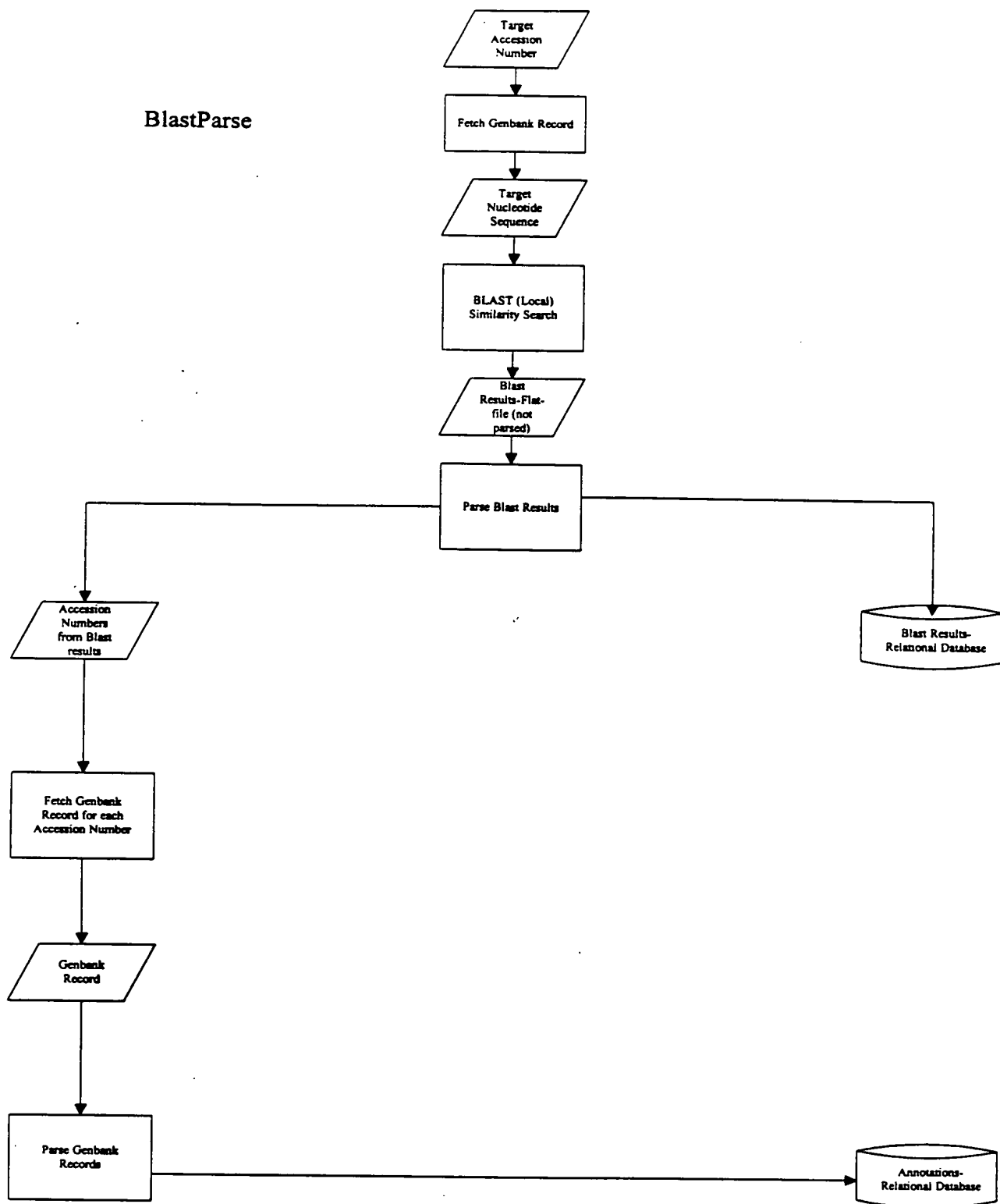


FIGURE 3

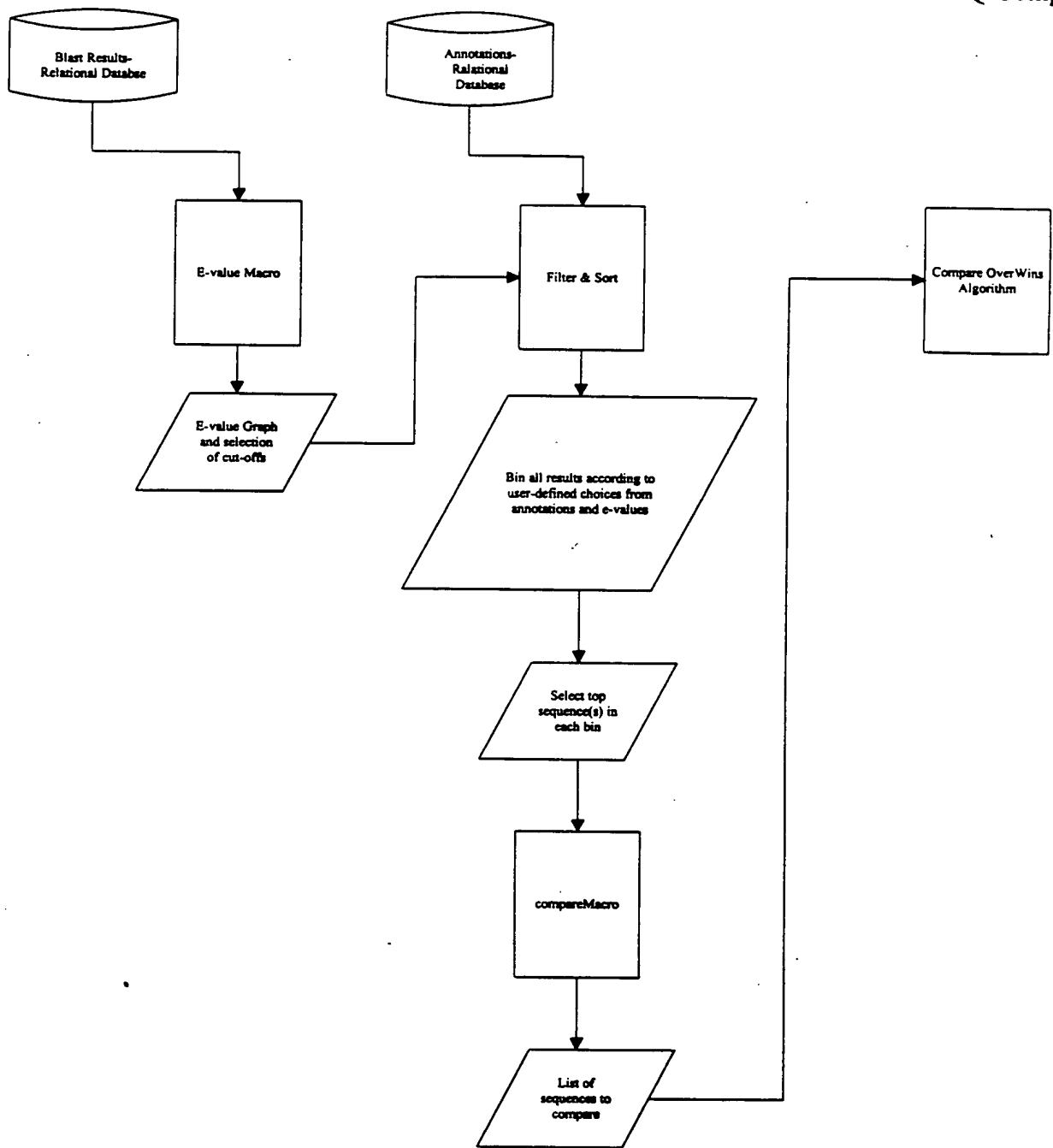


FIGURE 4

091057.051260
662750.79907660

CompareOverWins Algorithm Flow Chart

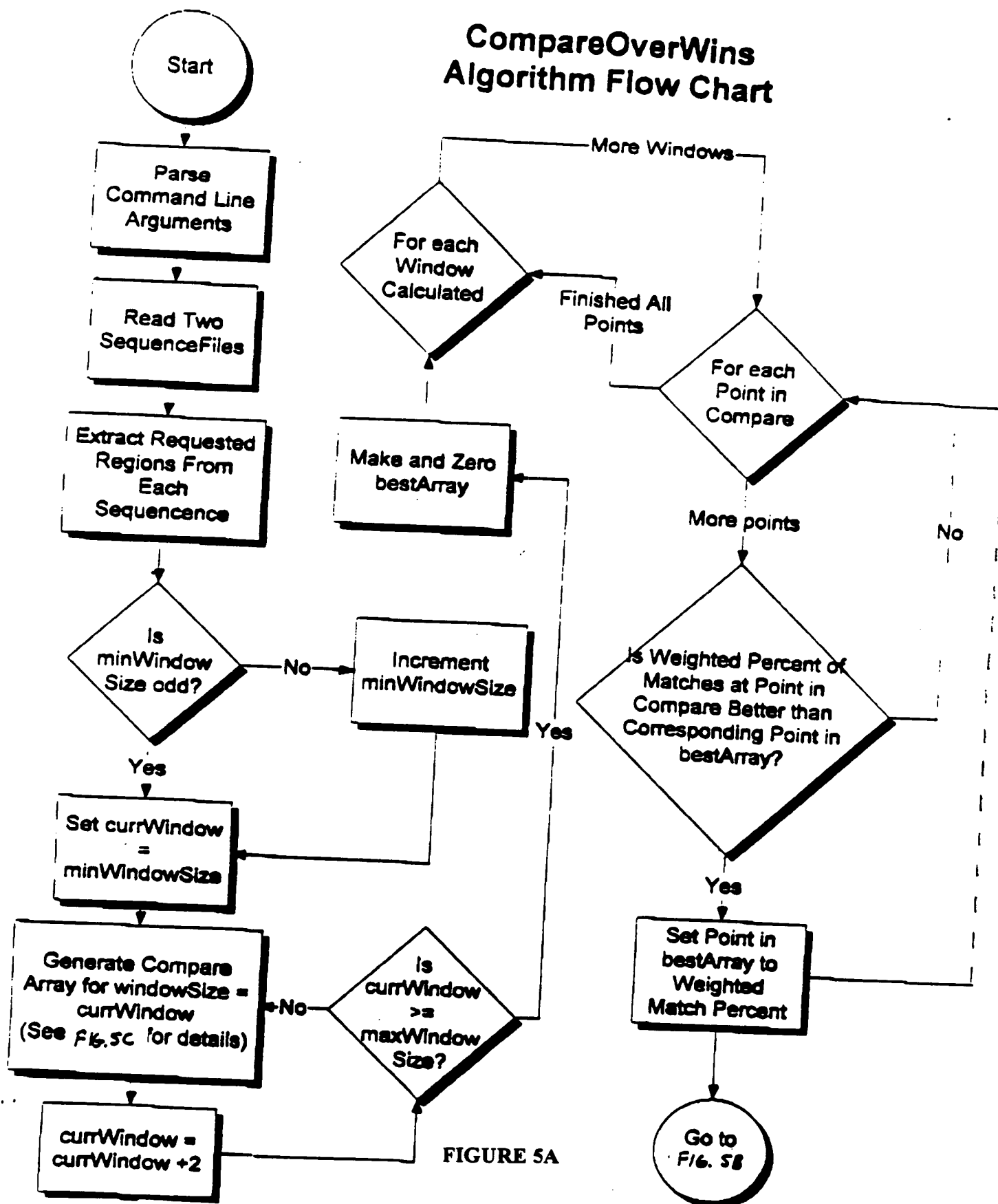
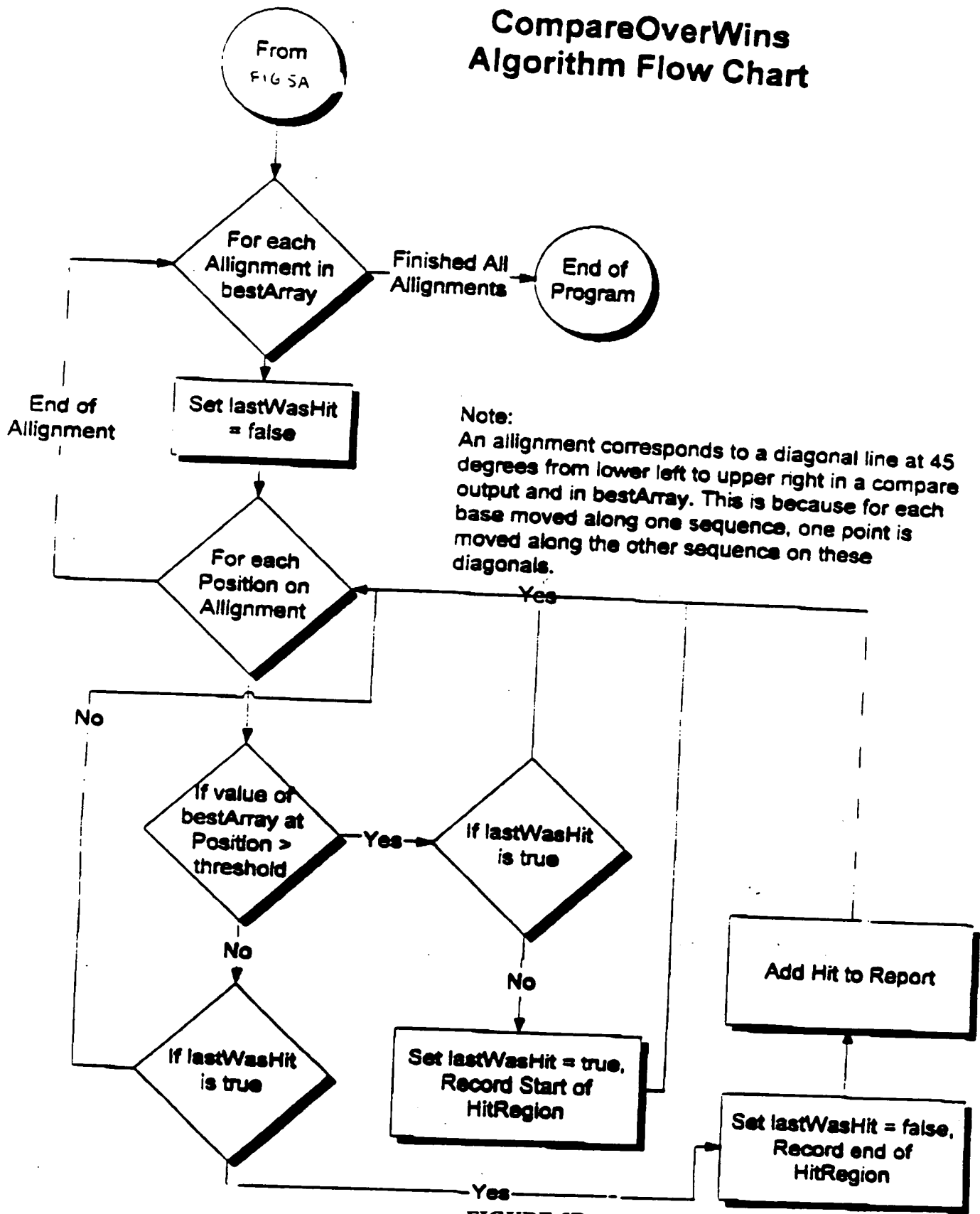


FIGURE 5A

00310667-051299

CompareOverWins Algorithm Flow Chart



00310567.051299

CompareOverWins Algorithm Flow Chart Basic Compare

Input:
Sequence A length a
Sequence B length b
Window Size

Output:
Array of size a by b of unsigned chars (0-255)
Each point represents the number of matches in the
window at that alignment and position

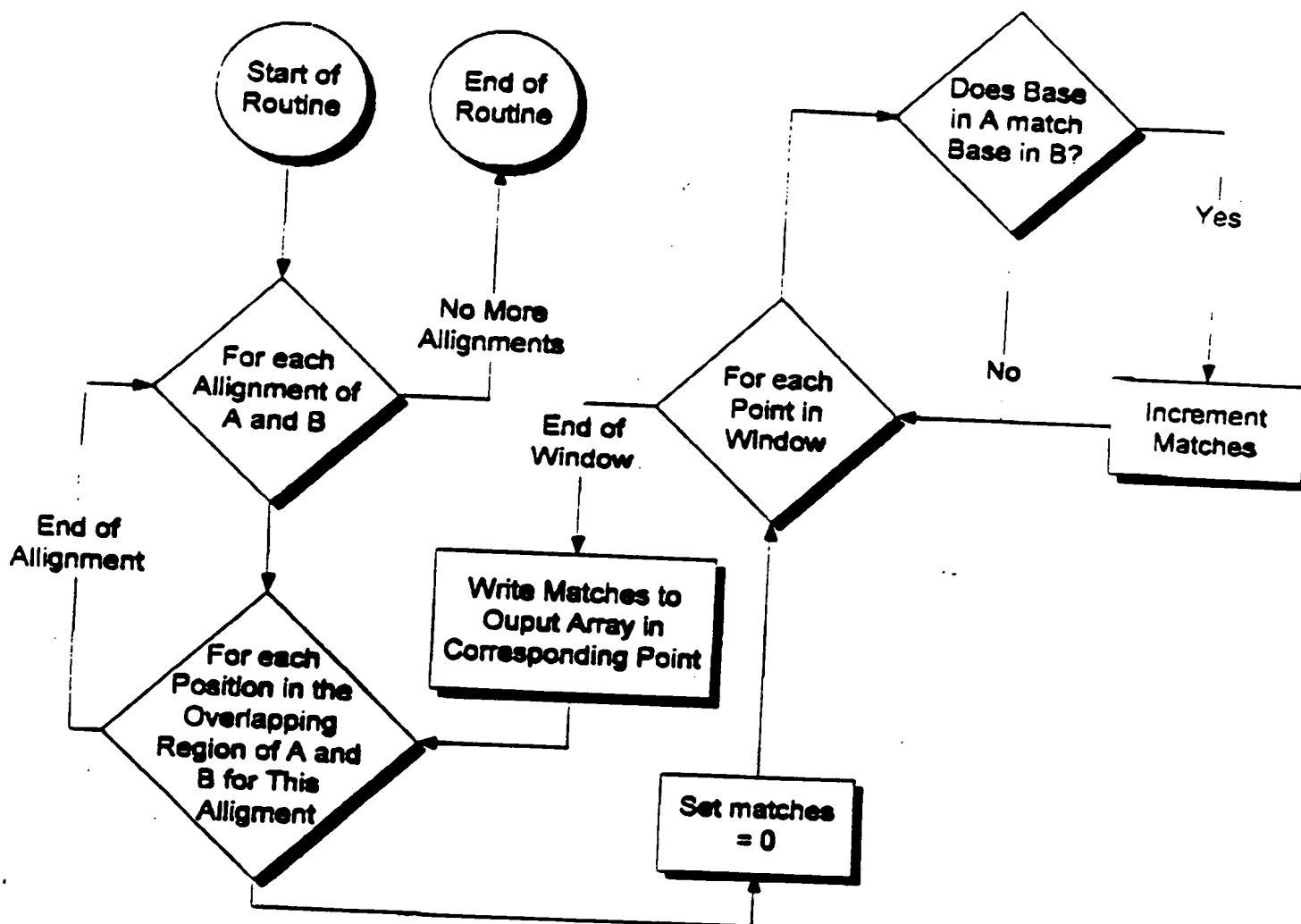
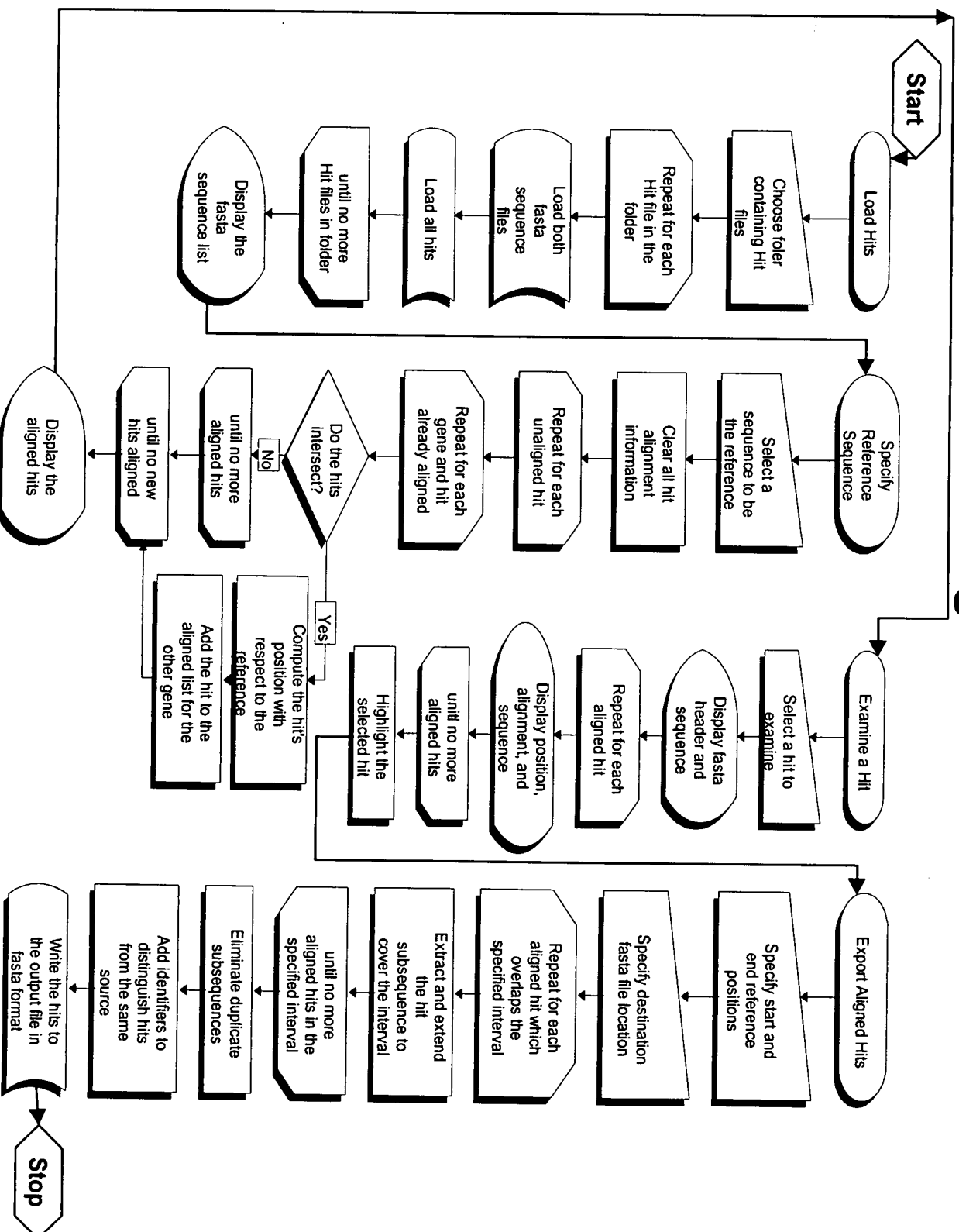


FIGURE 5C

09310667.051299

Fig. 5D



09310667.051299

Ferritin

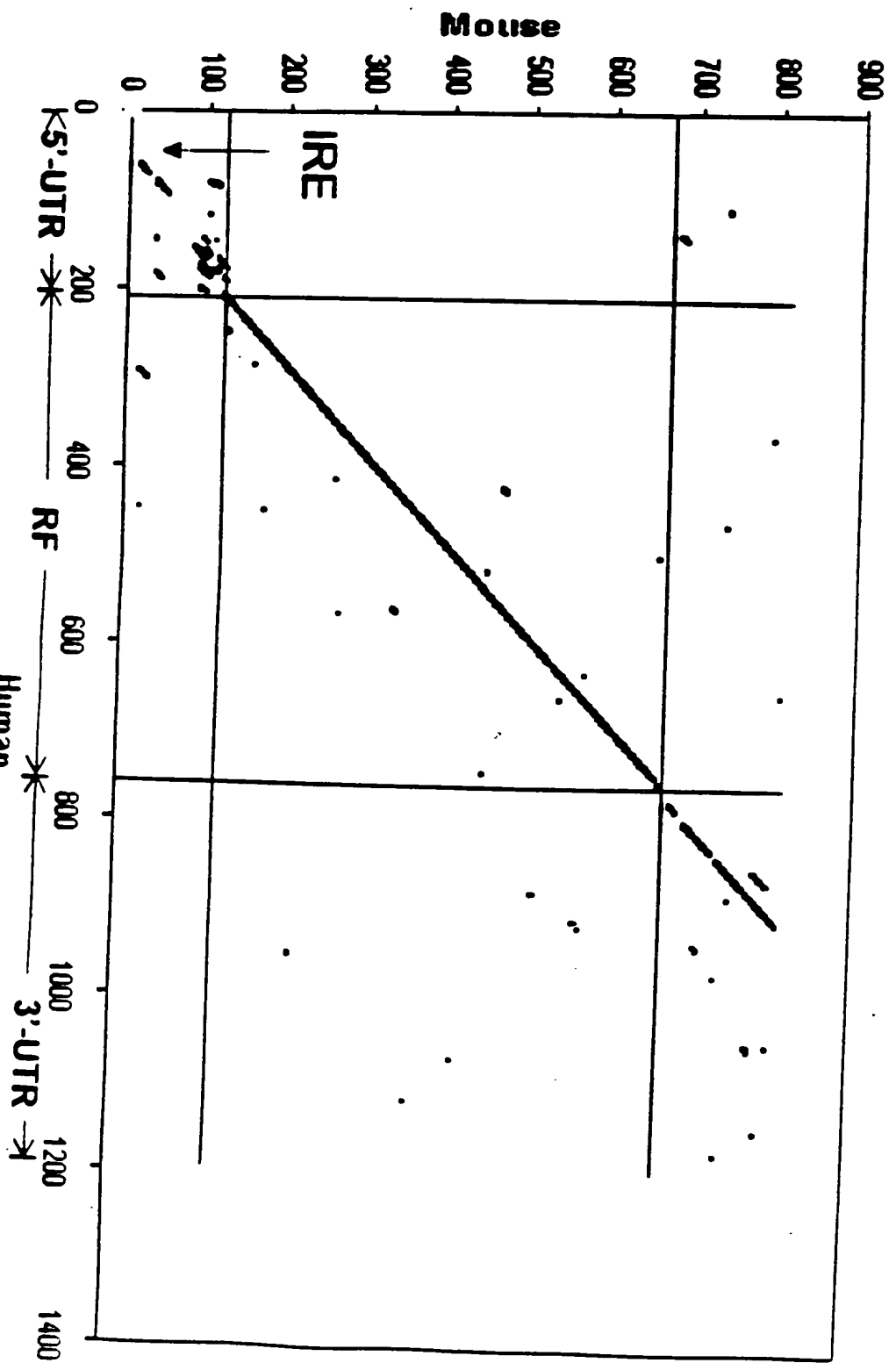
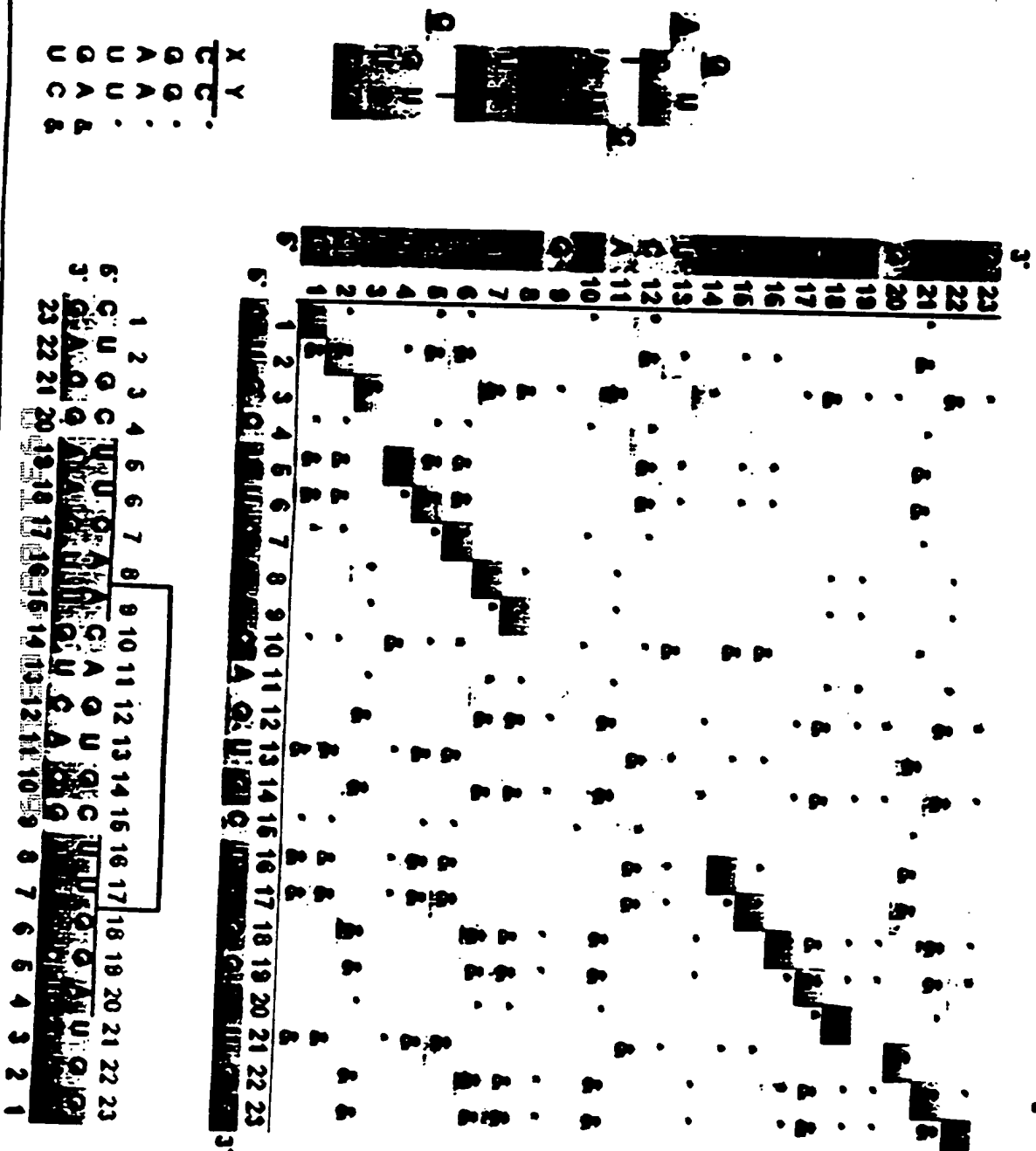


FIGURE 6

09310557.051299

Self Complementation Analysis - Single Sequence

FIGURE 7



Self Complementarity Comparisons 13 ortholog overlay

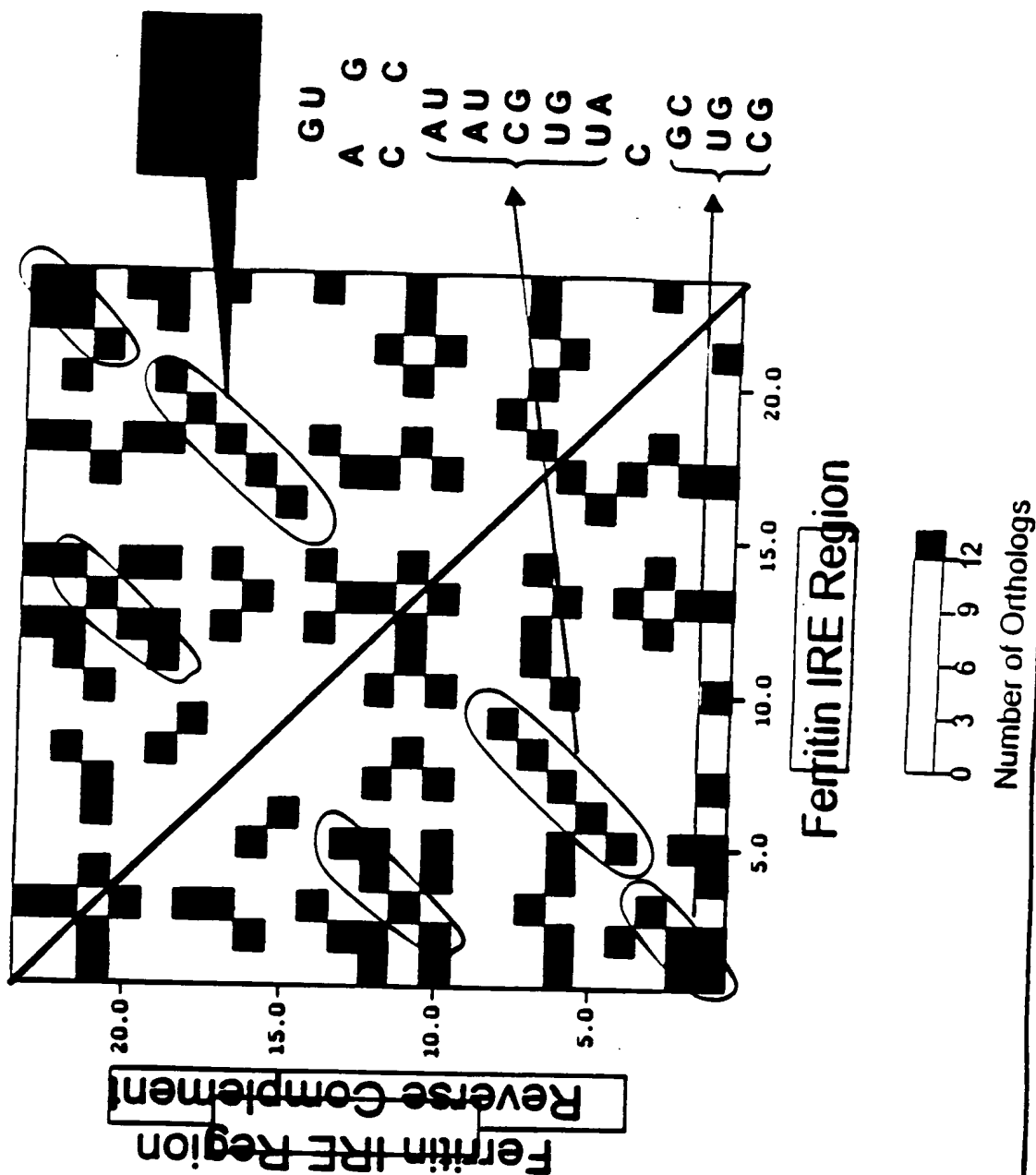
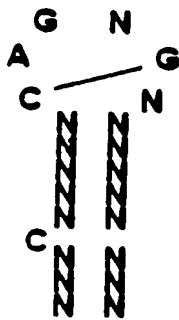


FIGURE 8

Typical Descriptor

This is an example of a descriptor used to identify iron response elements. To search the database using RNAMOT, the stem-loop model is converted to a text string as shown below:



IRE
Stem-loop
Model

H1 S1 H2 S2 H2 H1

H1 3:3 NNN:NNN

S1 1 C

H2 5:5 NNNNN:NNNNN

S2 6 CAGNGN

W2

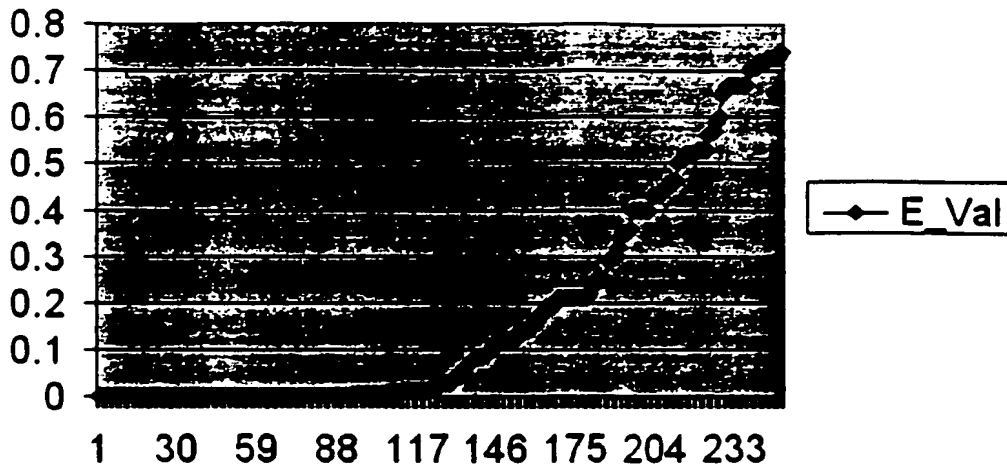
M0

IRE String descriptor

This descriptor allows for a wobble (W) of 2 (allows G-U pairing) and no mismatches. N can be any nucleotide. H refers to the stem region while S refers to the single stranded region.

FIGURE 9

E_Val



00310667 051299
662750 29907E60

FIGURE 10

662750° 29907E60

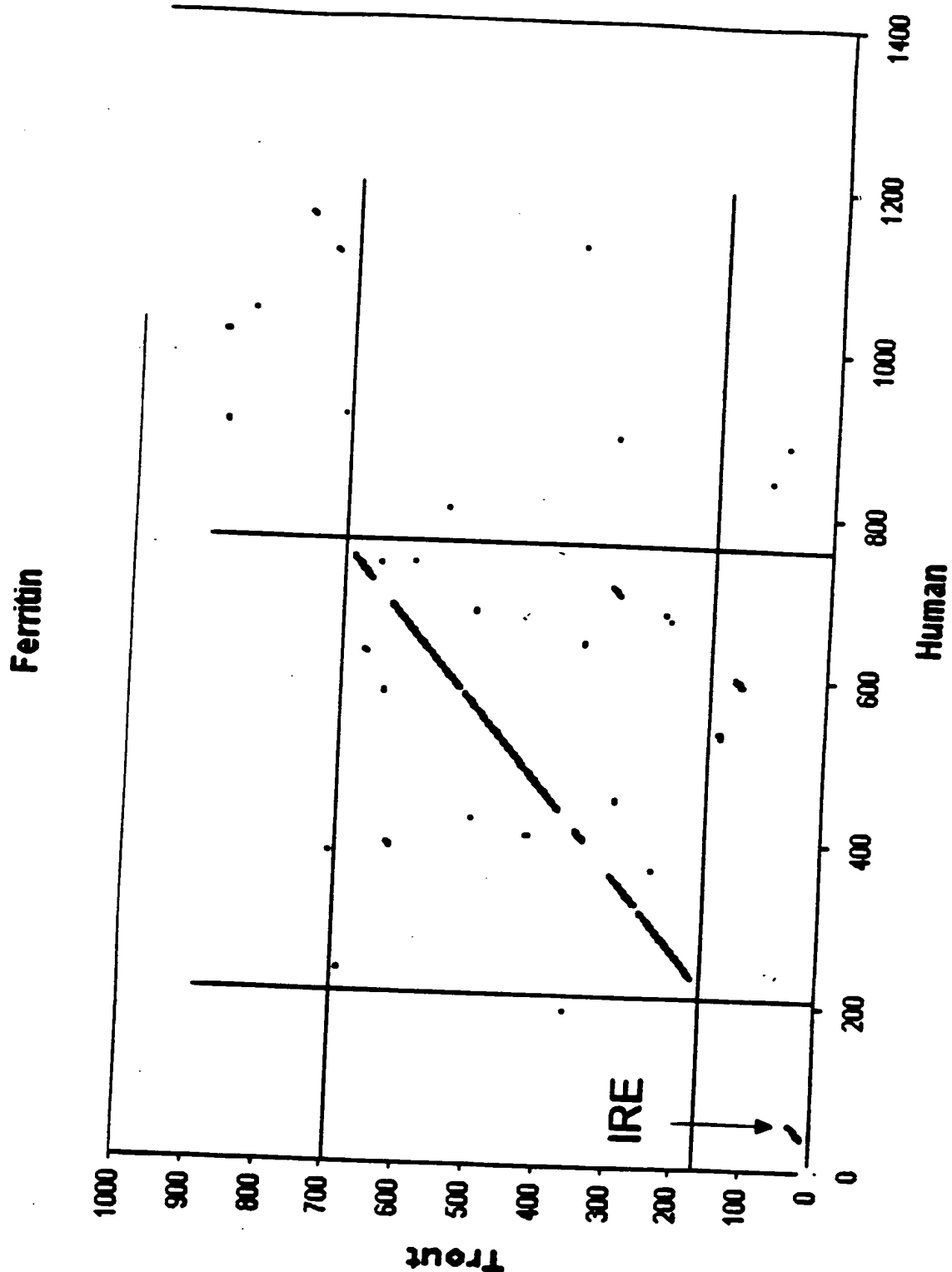


FIGURE 11

662T50-2990TE60

Ferritin

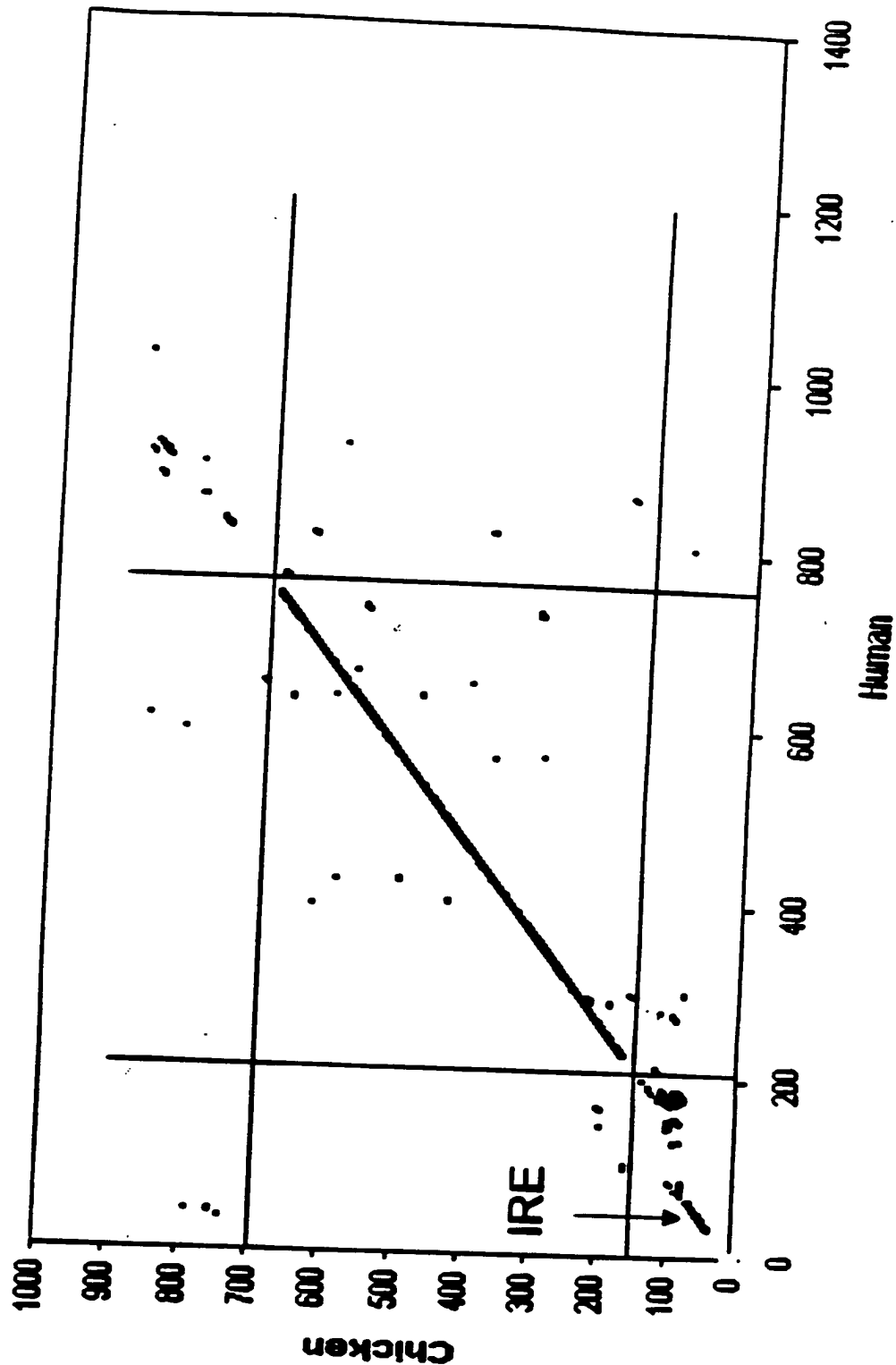


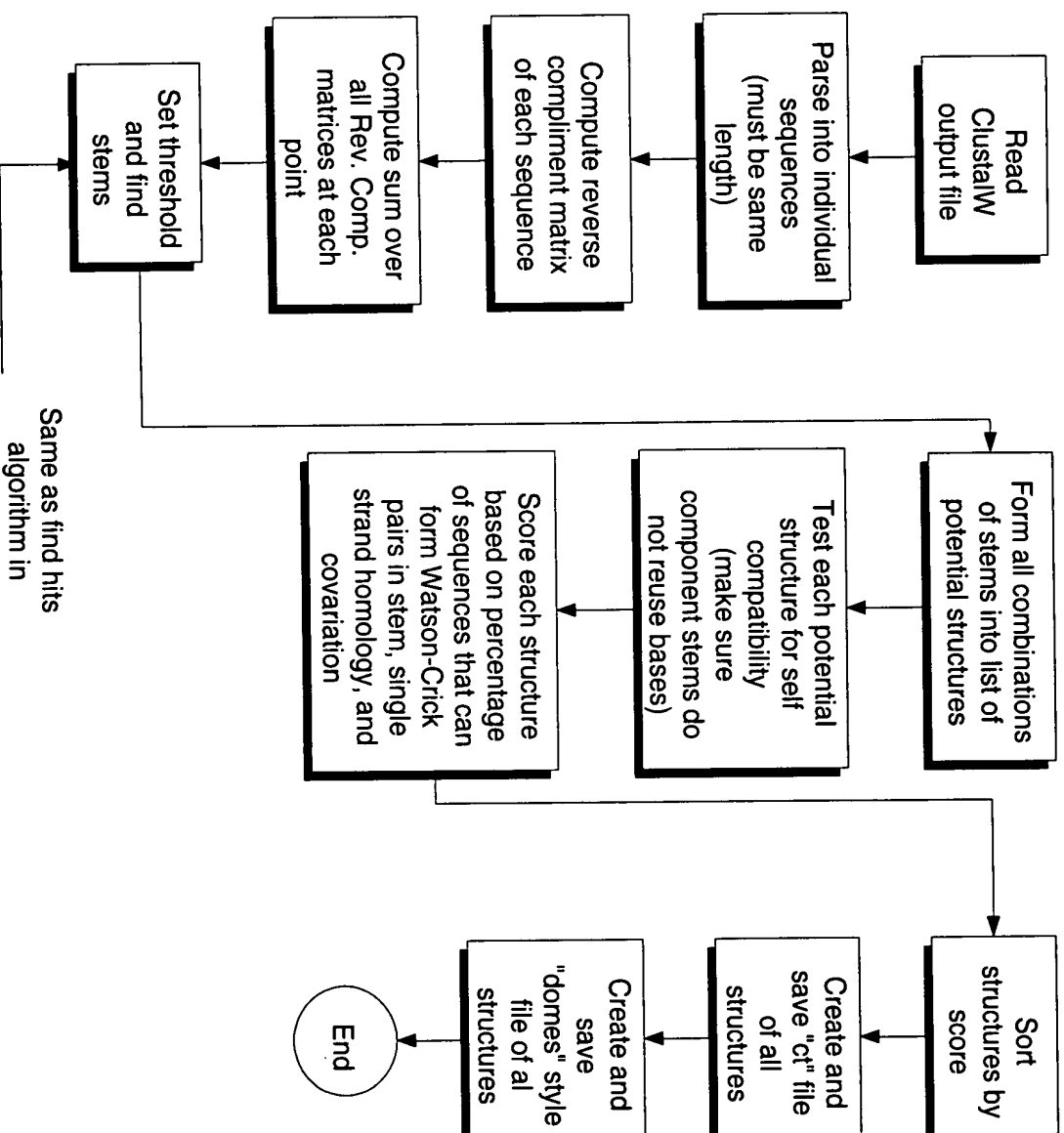
FIGURE 12

G-U A G G G U
 A C C C C C
 A-U A-U C-G U-G U-A C
 G-C U-G C-G
 HUMAN PIG
 G-U A G G G U
 A C C C C C
 A-U A-U C-G U-G U-A C
 G-C U-G C-G
 HAMSTER MOUSE
 G-U A G G G U
 A C C C C C
 A-U A-U C-G U-G U-A C
 G-C U-G C-G
 CHICKEN
 G-U A G G G U
 A C C C C C
 A-U A-U C-G U-G U-A C
 G-C U-G C-G
 TROUT SALMON
 G-U A G G G U
 A C C C C C
 A-U A-U C-G U-G U-A C
 G-C U-G C-G
 XENOPUS FROG
 G-U A G G G U
 A C C C C C
 A-U A-U C-G U-G U-A C
 G-C U-G C-G
 FLY
 G-U A G G G U
 A C C C C C
 A-U A-U C-G U-G U-A C
 G-C U-G C-G
 MOSQUITO

HUMAN PIG	HAMSTER MOUSE RAT	CHICKEN	TROUT SALMON	XENOPUS FROG	FLY	MOSQUITO
No	No	Yes	Yes	Yes	No	No
	No	Yes	Yes	Yes	No	No
		No	Yes	Yes	No	No
			No	Yes	Yes	Yes
				No	Yes	Yes
					No	Yes
						No

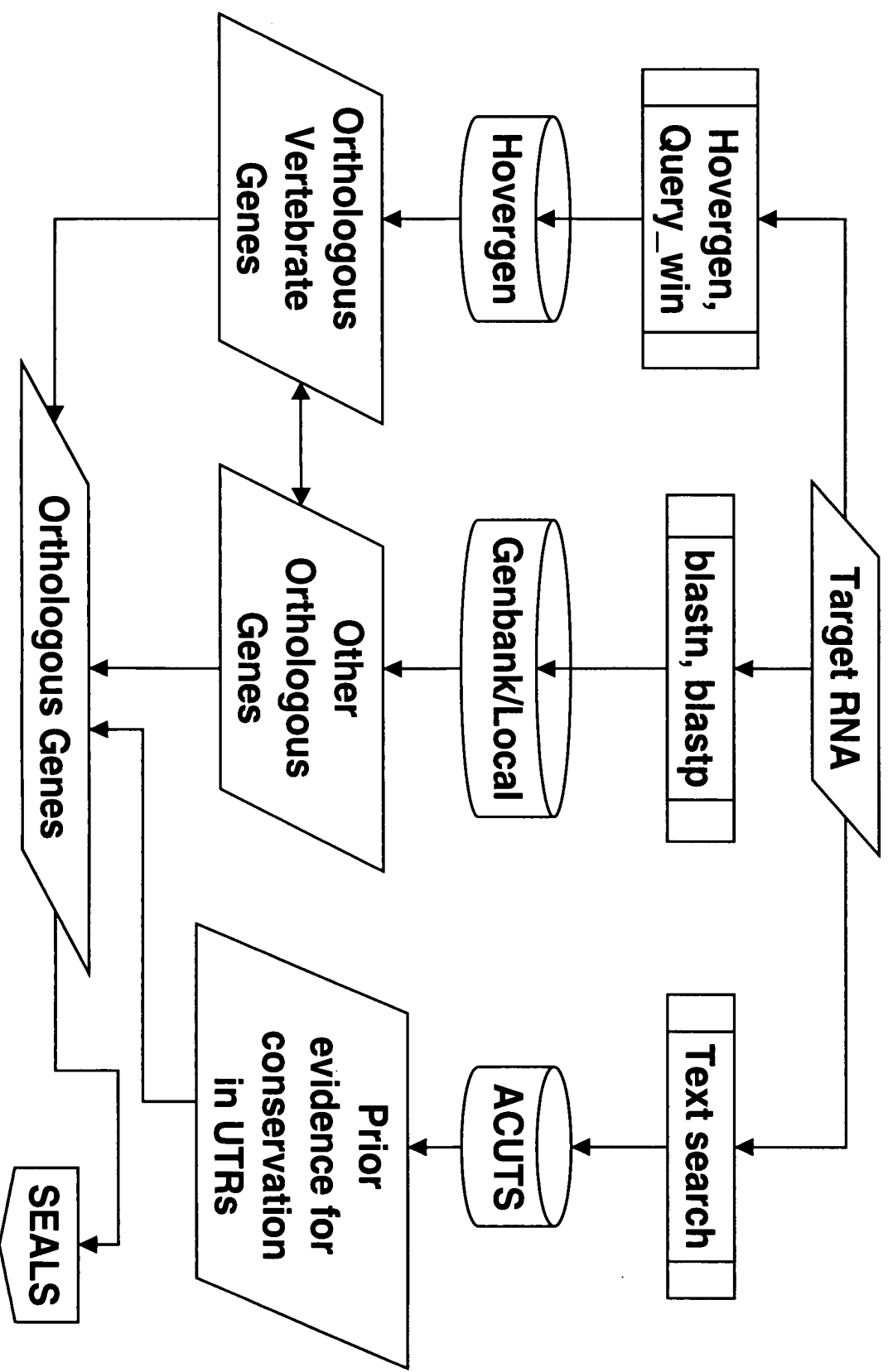
FIGURE 13

Figure 14



Same as find hits
algorithm in
Compare Over
Windows
09.31.05 12:49

Figure 15



ferritin H subunit



HOVERGEN
Homologous Vertebrate Gene Data Base

Warning: Phylogenetic trees are unrooted!
 Select a gene or node (N) as outgroup to position the root (option= "New outgroup")

Get info

Select for Alignment

Select for Output

New outgroup

Swap nodes

Sub- tree

Reset tree

tree display ...

miscellaneous ...

☐ Small leaf

☐ Branch lengths

tree display ...

miscellaneous ...

☐ Small leaf

☐ Branch lengths

Legend for Taxon Color

Hovergen color file : hovergen.col

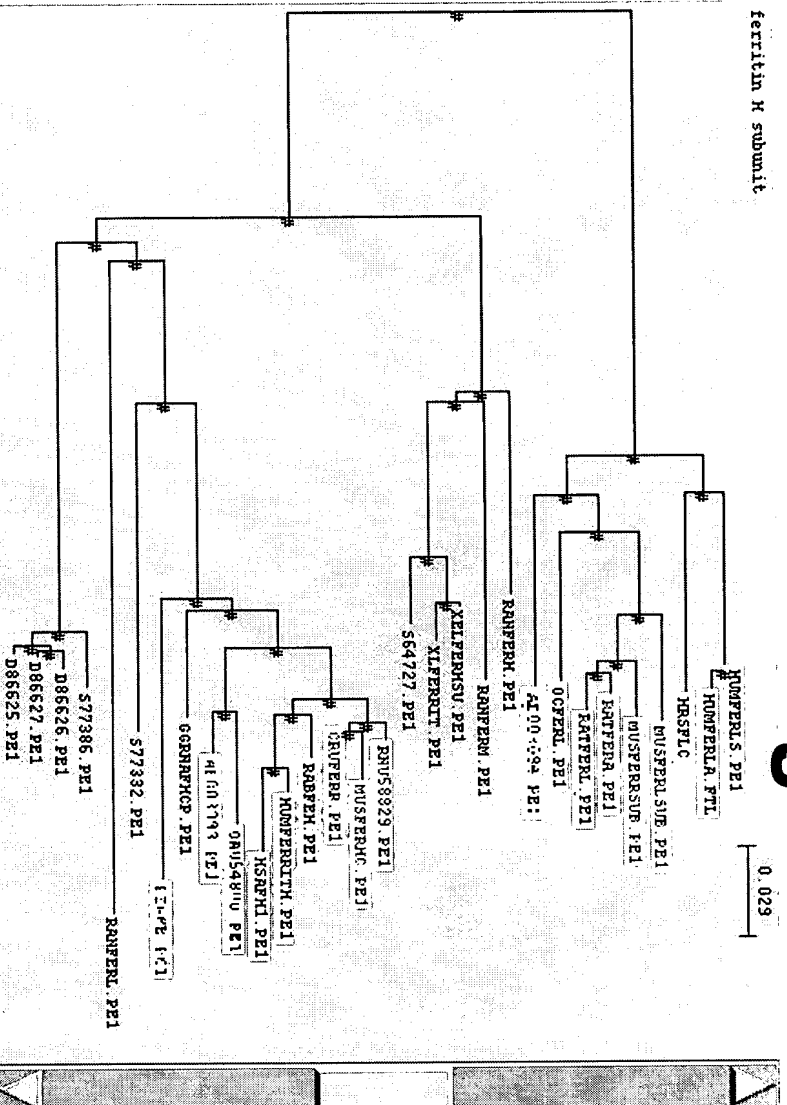
Change Color Set: [icon] [icon] [icon]

<input type="checkbox"/>	HOMO SAPIENS
<input type="checkbox"/>	MUS MUSCULUS
<input type="checkbox"/>	RATTUS NORVEGICUS
<input type="checkbox"/>	GALLUS GALLUS
<input type="checkbox"/>	BOS TAURUS
<input type="checkbox"/>	XENOPUS LAEVIS
<input type="checkbox"/>	OR YCTOLAGUS CUNICULUS
<input type="checkbox"/>	SUS SCROFA
<input type="checkbox"/>	CAVIA PORCELLUS
<input type="checkbox"/>	DANIO RERIO
<input type="checkbox"/>	OVIS ARIES
<input type="checkbox"/>	MAMMALIA
<input type="checkbox"/>	Other

species: [icon] [icon] [icon]

Apply

Figure 17



09310667-051693

HOMOGYEN <i>Homologous Vertebrate Genes Data Base</i>	
<p>Warning: Phylogenetic trees are unrooted! Select a gene or node (#) as outgroup to position the root (option= "New outgroup")</p>	
<ul style="list-style-type: none"> <input type="checkbox"/> Get info <input checked="" type="checkbox"/> Select for Alignment <input checked="" type="checkbox"/> Select for Output <input type="checkbox"/> New outgroup <input type="checkbox"/> Swap nodes <input type="checkbox"/> Sub - tree <input type="checkbox"/> Root tree 	<div style="border: 1px solid black; padding: 5px; margin-bottom: 5px;"> <input type="checkbox"/> Small leaf </div> <div style="border: 1px solid black; padding: 5px;"> <input type="checkbox"/> Branch lengths </div>
<div style="border: 1px solid black; padding: 5px; margin-bottom: 5px;">tree display ...</div> <div style="border: 1px solid black; padding: 5px;">miscellaneous ...</div>	<div style="border: 1px solid black; padding: 5px; margin-bottom: 5px;"> <input type="checkbox"/> New Tree </div> <div style="border: 1px solid black; padding: 5px;"> <input type="checkbox"/> </div>
<div style="display: flex; justify-content: space-between;"> Legend for Taxon Color mammalian orders </div>	
<p>Howgen color file :</p> <div style="border: 1px solid black; height: 20px; width: 100%;"></div> <p>hovgen.colof</p>	<p>Change Color Set</p> <div style="border: 1px solid black; padding: 5px;"> <input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/> </div>
<div style="border: 1px solid black; padding: 5px;"> <input type="checkbox"/> PRIMATES <input type="checkbox"/> RODENTIA <input type="checkbox"/> ARTIODACTYLA <input type="checkbox"/> LAGOMORPHA <input type="checkbox"/> CARNIVORA <input type="checkbox"/> CETACEA <input type="checkbox"/> PERISSODACTYLA <input type="checkbox"/> CHIROPTERA <input type="checkbox"/> INSECTIVORA <input type="checkbox"/> MONOTREMATA <input type="checkbox"/> EDENTATA <input type="checkbox"/> MAMMALIA <input type="checkbox"/> Other: </div>	<div style="border: 1px solid black; padding: 5px;"> <input type="checkbox"/> Apply </div>
<div style="display: flex; align-items: center;"> <input type="checkbox"/> auto </div>	

Figure 18

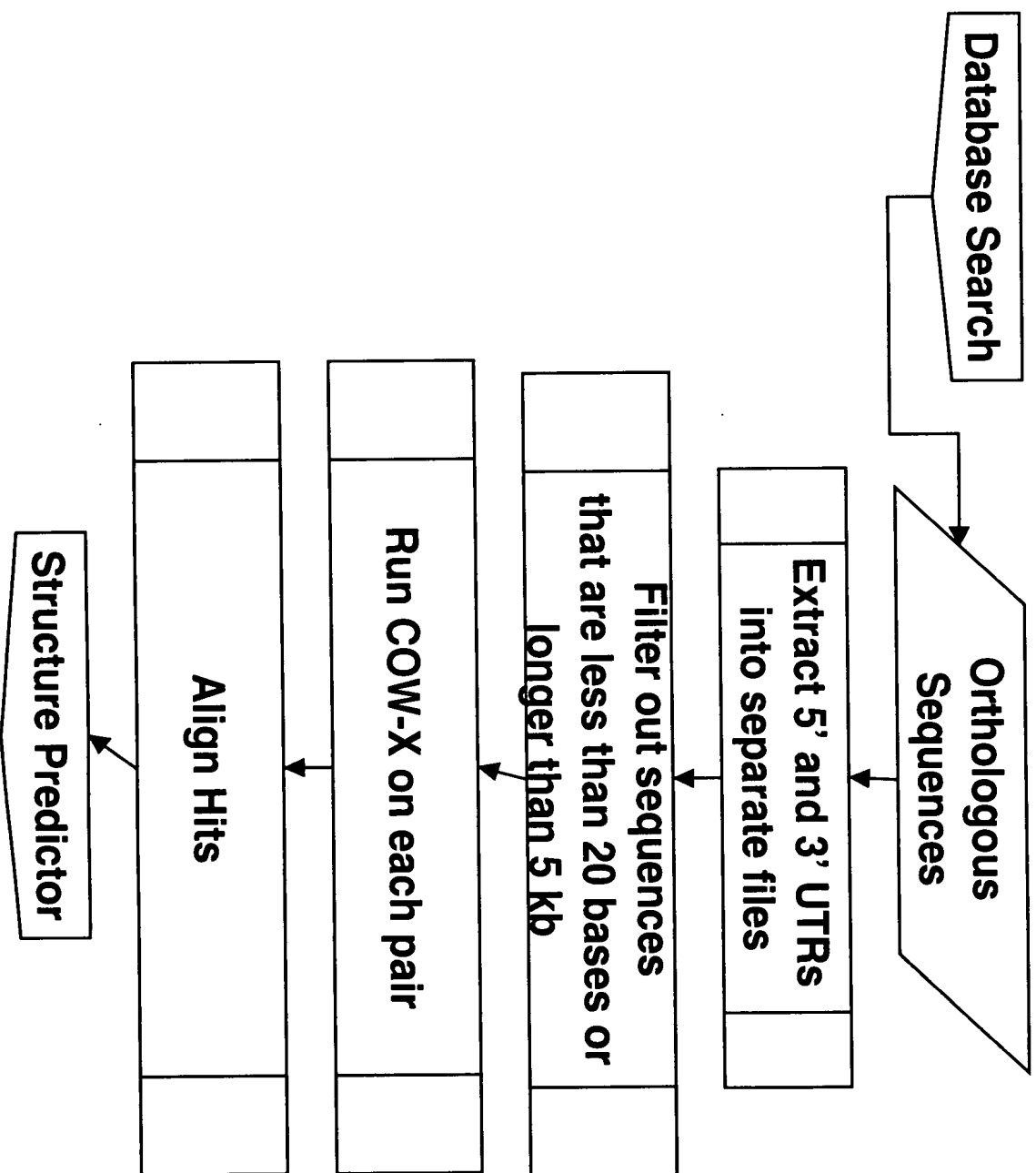


Figure 19

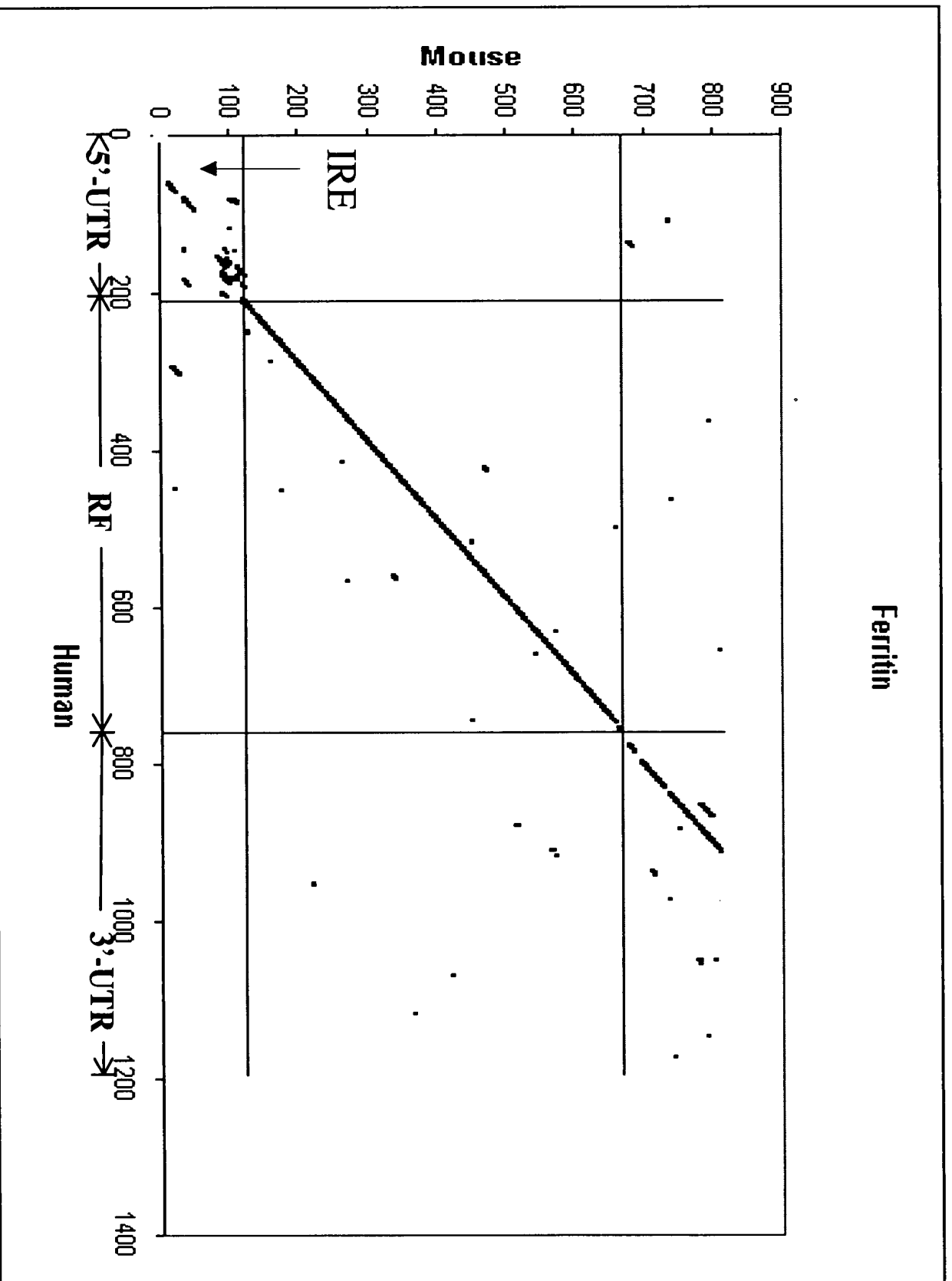


Figure 20

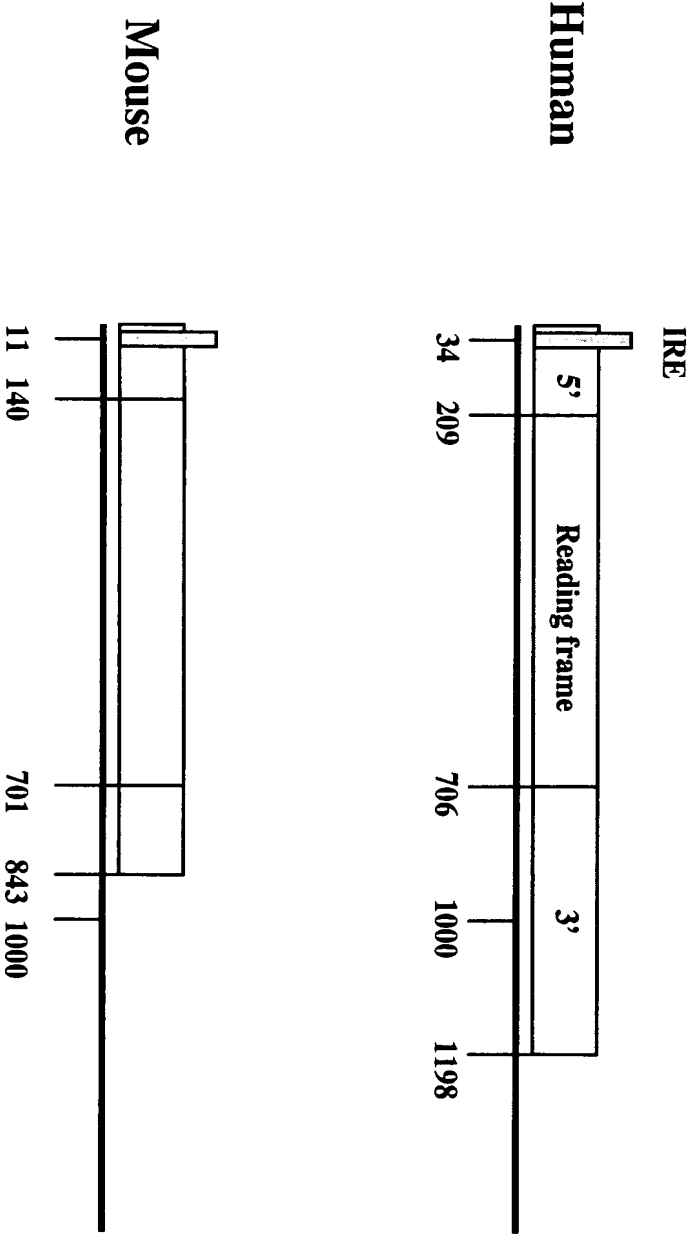


Figure 21

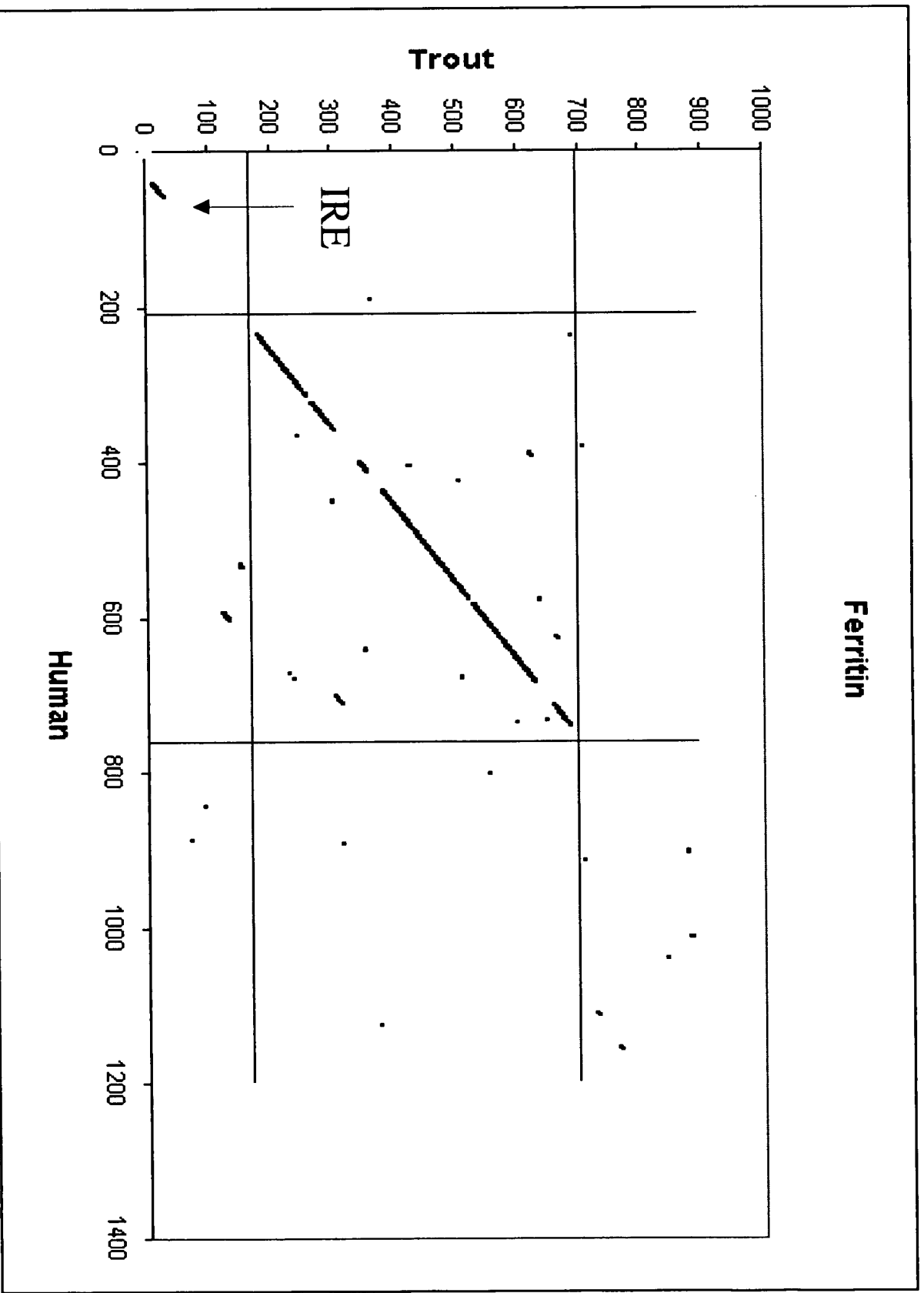


Figure 22

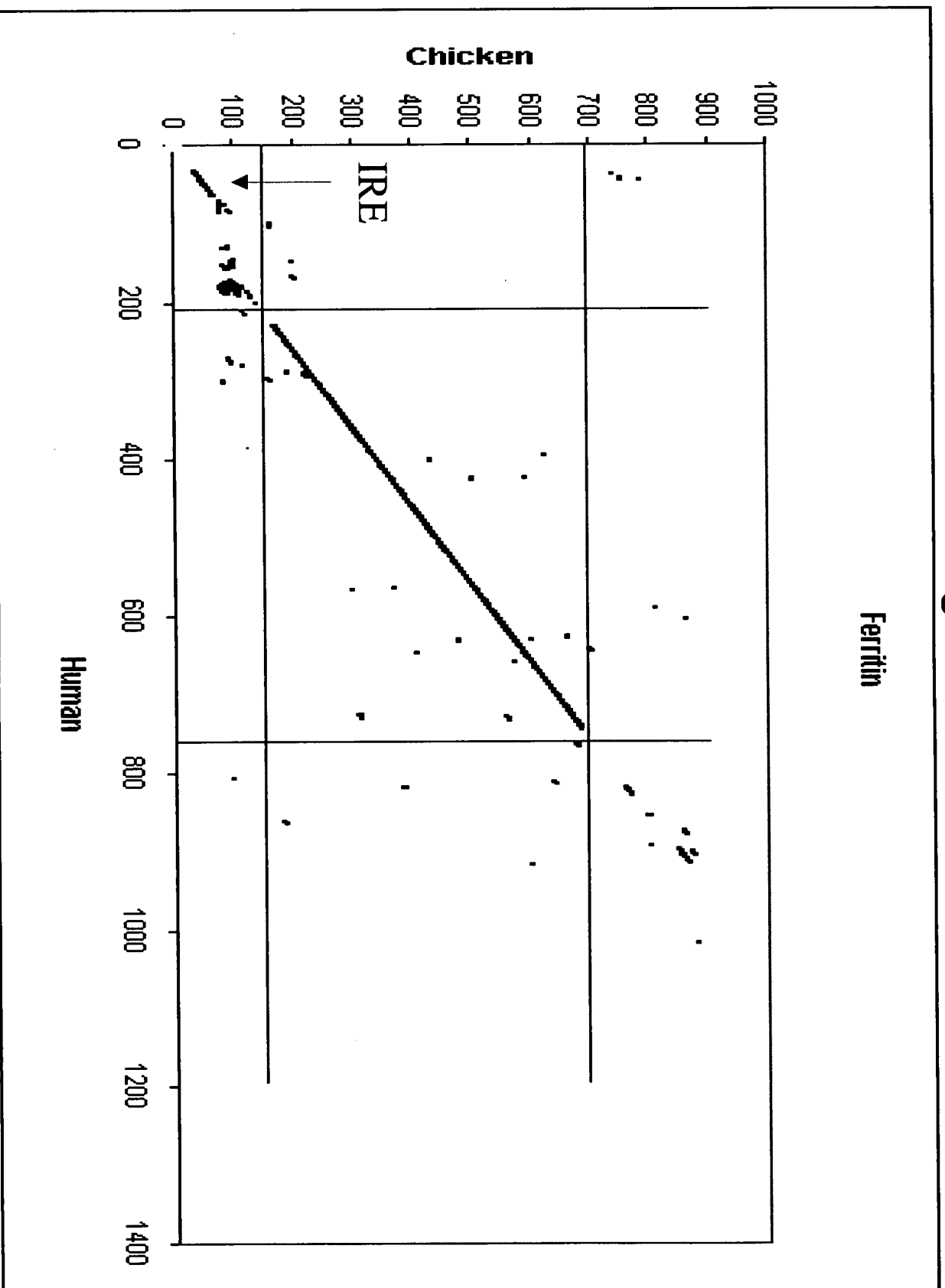
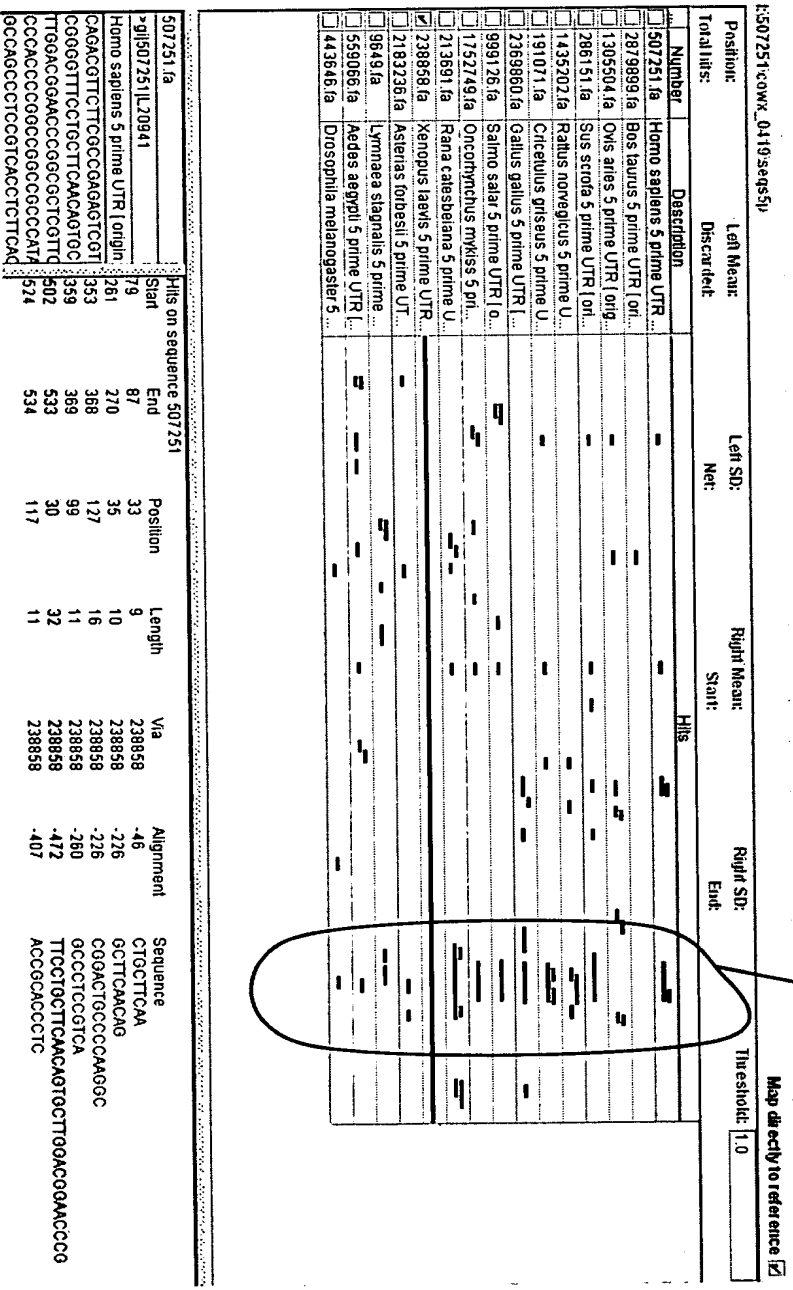


Figure 23

Conserved Region



09310657 051299

Figure 24

5p_xenopus_500_535_auto.aln [Read-Only]		A	
1	CLUSTAL W (1.74) multiple sequence alignment		
2			
3			
4	gi 1752749 D86626	AGAAAGTTGCTTC AACAGTGATTGAAACGGAACCTCCTC-	
5	gi 999126 S77386	AGTTCTTGCTTC AACAGTGATTGAAACGGAACCTCCTC-	
6	gi 213691 M12120	AGTTCTTGCTTC AACAGTGTTGAAACGGAAC-CCTCT	
7	gi 238858 S64727	AGTTCTTGCTTC AACAGTGTTGAAACGGAAC-CCTCT	
8	gi 286151 D15071	GTTTCCTGCTTC AACAGTGCTTGGAACGGAACCCGGC-	
9	gi 507251 L20941	GTTTCCTGCTTC AACAGTGCTTGGAACGGAACCCGGC-	
10	gi 191071 M99692	GTTTCCTGCTTC AACAGTGCTTGGAACGGAACCCGGC-	
11	gi 2369860 Y14698	GGTTCCTGCGTCAACAGTGCTTGGAACGGAACCCGGC-	
12		*** ***** *	
13			
14			
15			

Figure 25

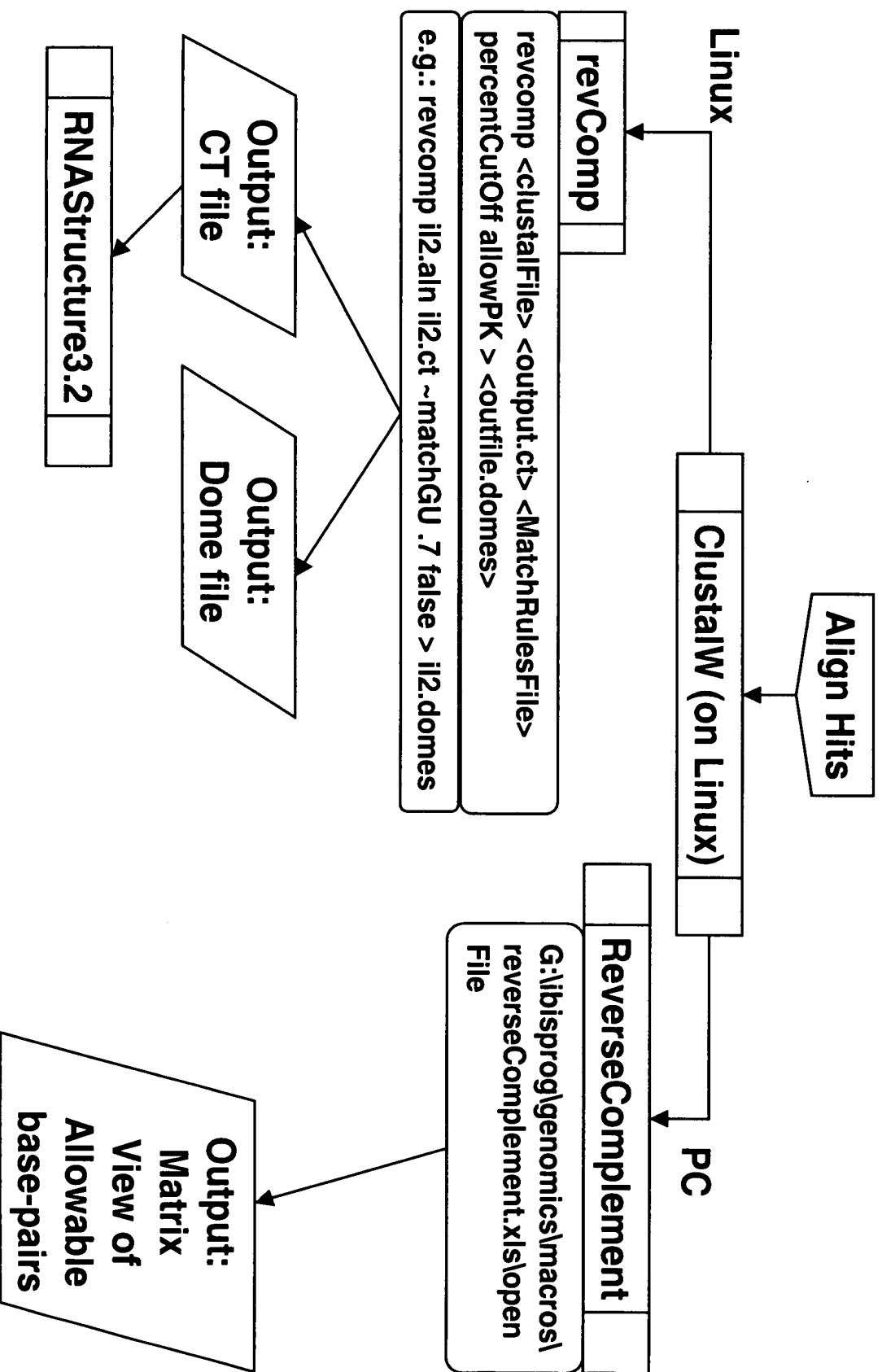


Figure 26

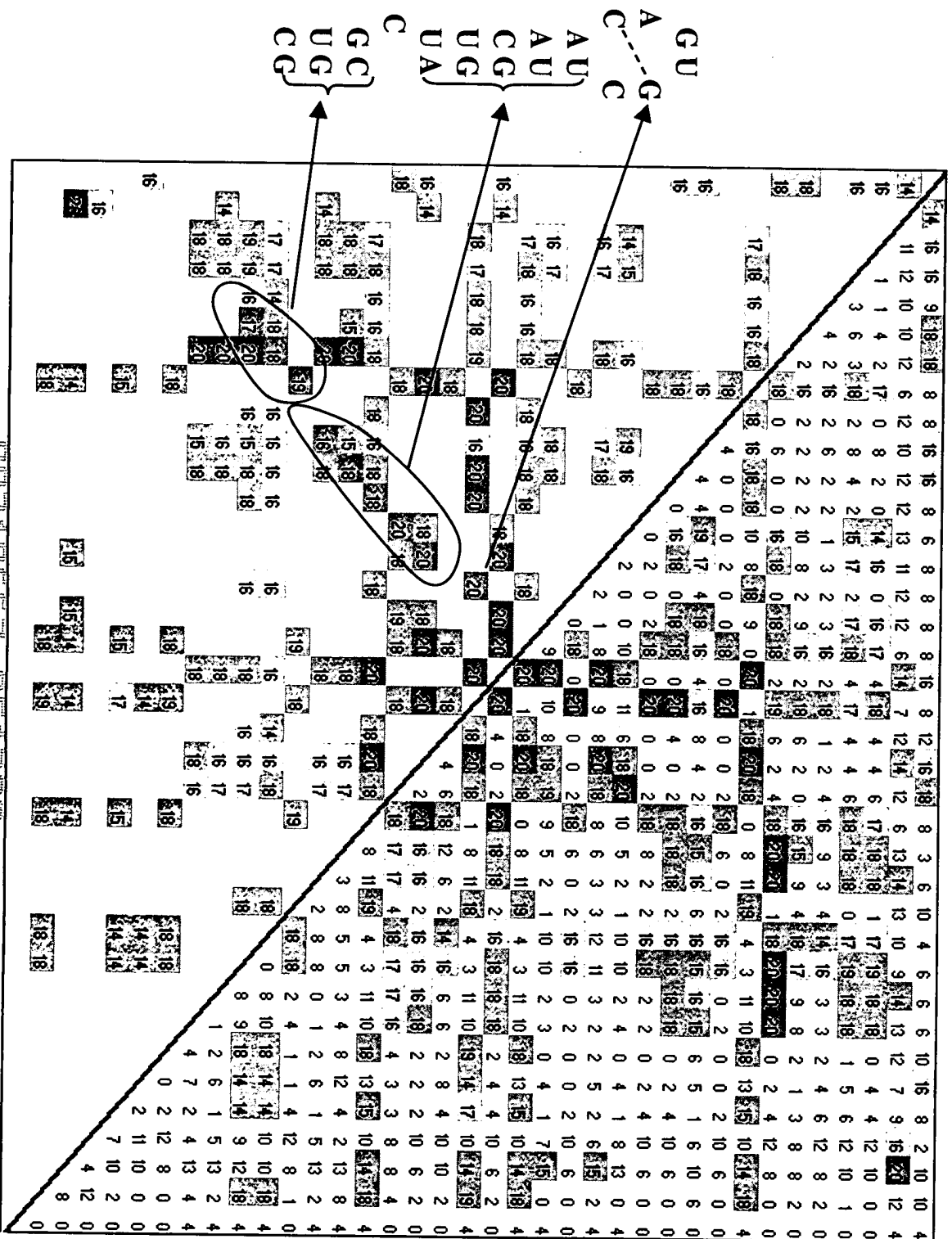
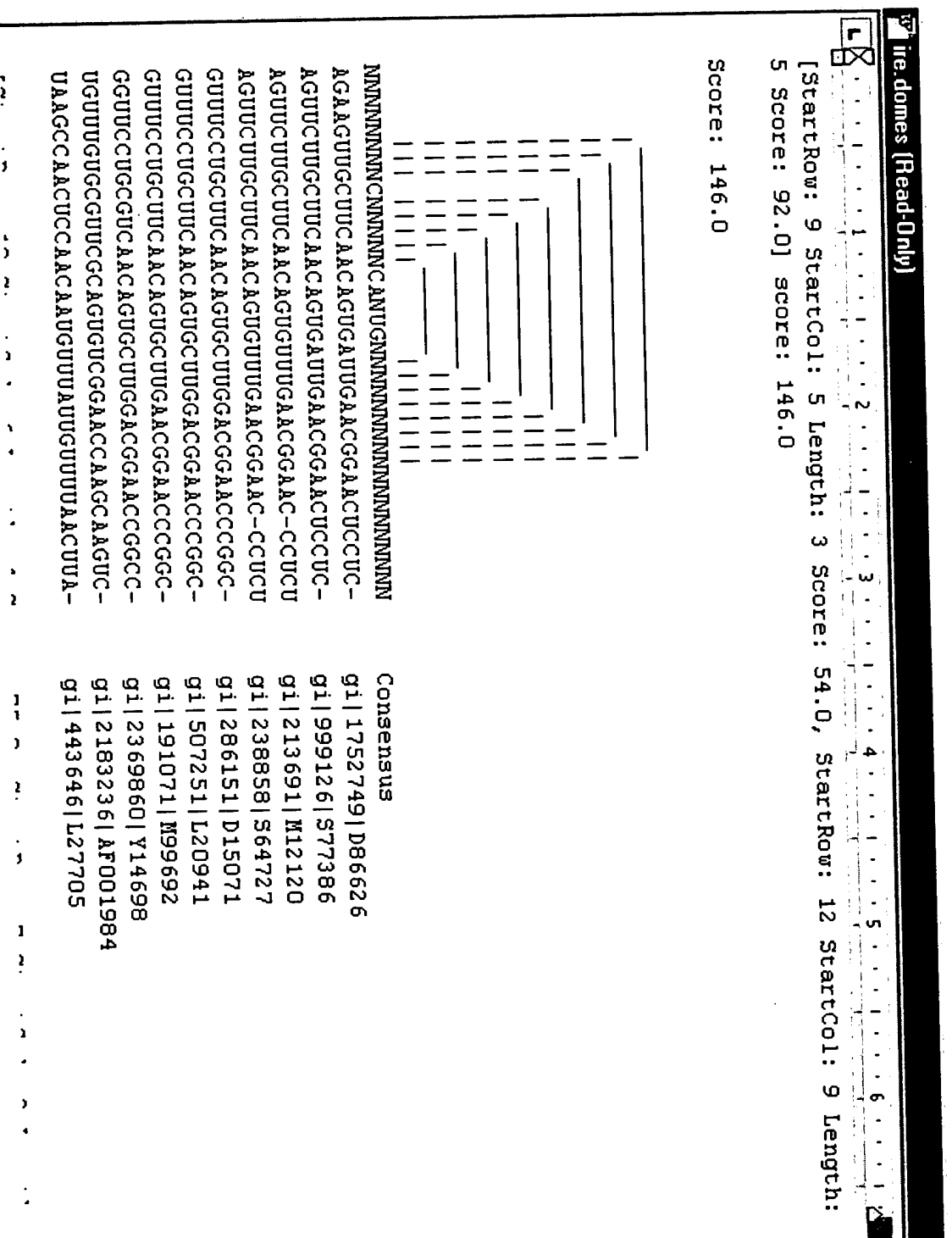


Figure 27



09310667.051299

Figure 28

IRE Structures for each species

	<div><div>G-U</div><div>A G</div><div>C C</div></div>	<div><div>G-U</div><div>A G</div><div>C C</div></div>	<div><div>G-U</div><div>A G</div><div>C C</div></div>	<div><div>G-U</div><div>A G</div><div>C A</div></div>	<div><div>G-U</div><div>A G</div><div>C U</div></div>	<div><div>G U</div><div>A G</div><div>C U</div></div>	<div><div>G U</div><div>A G</div><div>C U</div></div>
	<div><div>A-U</div><div>A-U</div><div>C-G</div><div>U-G</div><div>U-A</div></div>	<div><div>A-U</div><div>A-U</div><div>C-G</div><div>U-A</div><div>U-A</div></div>	<div><div>A-U</div><div>A-U</div><div>C-G</div><div>U-G</div><div>G-A</div></div>	<div><div>A-U</div><div>A-U</div><div>C-G</div><div>U-A</div><div>U-A</div></div>	<div><div>A-U</div><div>A-U</div><div>C-G</div><div>U-A</div><div>U-A</div></div>	<div><div>A-U</div><div>A-U</div><div>C-G</div><div>U-A</div><div>U-A</div></div>	<div><div>C-G</div><div>G-U</div><div>C-G</div><div>G-U</div><div>U-A</div></div>
	<div><div>C</div><div>G-C</div><div>U-G</div><div>C-G</div></div>	<div><div>C</div><div>G-C</div><div>U-G</div><div>C-G</div></div>	<div><div>C</div><div>G-C</div><div>U-G</div><div>C-G</div></div>	<div><div>C</div><div>G-C</div><div>U-G</div><div>U-G</div></div>	<div><div>C</div><div>G-C</div><div>U-G</div><div>U-G</div></div>	<div><div>C</div><div>G-C</div><div>U-A</div><div>U-A</div></div>	<div><div>C</div><div>U-A</div><div>U-A</div><div>C-G</div></div>
HUMAN		HAMSTER	CHICKEN	TROUT	XENOPUS	FLY	MOSQUITO
PIG		MOUSE		SALMON	FROG		
		RAT					

histones H1

☒ Append

Sequence Definition

output filename:

Save Info

09310667 051299

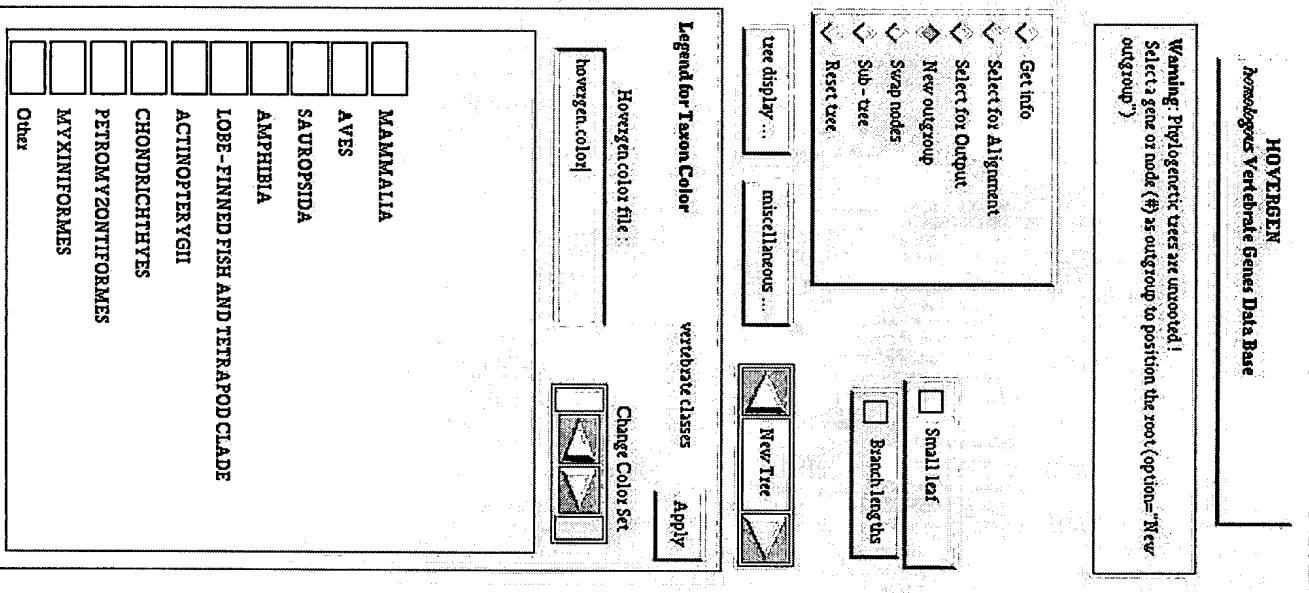


Figure 31

Conserved Region

E:\HISTONE\cowx_0416\seqs3p

Position:		Left/Meant:		Left/SD:	
Total hits:		Discarded:		Net:	
...	Number	Description	Hits		
<input type="checkbox"/>	63477.fa	Gallus gallus 3 prime UTR [...	—		
<input type="checkbox"/>	9788.fa	Pisaster brevispinus 3 prime...	—		
<input type="checkbox"/>	349586.fa	Volvox carteri 3 prime UTR [...	—		
<input type="checkbox"/>	10044.fa	Pisaster ochraceus 3 prime ...	—		
<input type="checkbox"/>	9989.fa	Pycnopodia helianthoides 3 ...	—		
<input checked="" type="checkbox"/>	161381.fa	Psammochinus miliaris 3 pr...	—		
<input type="checkbox"/>	9614.fa	Lytechinus pictus 3 prime U...	—		
<input type="checkbox"/>	31967.fa	Homo sapiens 3 prime UTR ...	—		
<input type="checkbox"/>	64766.fa	Xenopus laevis 3 prime UTR...	—		
<input type="checkbox"/>	404465.fa	Styela plicata 3 prime UTR [...	—		
<input type="checkbox"/>	342113.fa	Macaca mulatta 3 prime UT...	—		
<input type="checkbox"/>	797284.fa	Paracentrotus lividus 3 prim...	—		
<input type="checkbox"/>	287651.fa	Rattus norvegicus 3 prime U...	—		
<input type="checkbox"/>	2292939.fa	Mus musculus 3 prime UTR ...	—		
<input type="checkbox"/>	62730.fa	Cairina moschata 3 prime U...	—		
<input type="checkbox"/>	10251.fa	Strongylocentrotus purpuratu...	—		
<input type="checkbox"/>	62440.fa	Anas platyrhynchos 3 prime ...	—		
<input type="checkbox"/>	10338.fa	Solaster stimpsoni 3 prime ...	—		
<input type="checkbox"/>	515003.fa	Mus pahari 3 prime UTR [ori...	—		

Figure 32

3p_xenopus_23_56_autoaln [Read-Only]

A	
1	CLUSTAL W (1.74) multiple sequence alignment
2	
3	
4	gi 10044 X54113 -TAAACAAAACGGCTCTTTTCAGAGCCACCACTTC-
5	gi 9788 X54112 -TAAACAAAACGGCTCTTTTCAGAGCCACCACTTC-
6	gi 9989 X54114 -TAATCAAAAACGGCTCTTTTCAGAGCCACCACTTC-
7	gi 10251 V01356 ATACACAAA-CGGCTCTTTTCAGAGCCACCAACAAC-
8	gi 161381 M10558 ATACACAAA-CGGCTCTTTTCAGAGCCACCAACAAC-
9	gi 9614 X00628 TAACCAAAA-CGGCTCTTTTCAGAGCCACCAATAAC-
10	gi 404465 S64499 -GACACAAAACGGCTCTTTTCAGAGCCACCA-ATCG
11	gi 31967 X57129 AAACCCA-AAAGGCTCTTTTCAGAGCCACCACTGA-
12	gi 515003 X80327 -CCCCACAAAAGGCTCTTTTCAGAGCCACCACTGC-
13	gi 2292939 Y12291 -CAATCCAAAAGGCTCTTTTCAGAGCCACCACTCC-
14	gi 287651 X67320 -ACAACCCAAAAGGCTCTTTTCAGAGCCACCAACAA-
15	gi 342113 M97756 -AGAACCCAAAAGGCTCTTTTAAGAGCCACCAACCAT-
16	gi 63477 X01752 -GATATCCAAACGGCTCTTTTAAGAGCCACCAACACAC-
17	gi 64766 X03017 -TATACCCAAAAGGCTCTTTTCAGAGCCACCAACCC-
18	gi 62440 X06128 -TAAACCCAAAAGGCTCTTTTAAGAGCCACCAACCACTT-
19	gi 62730 X14731 -TTAACCCAAAAGGCTCTTTTCAGAGCCACCAACCACTT-
20	gi 10338 X54115 -CAAACCGAAGCGCCCTTTTAGGCCACTACACTTT-
21	* * * * *
22	NNNNNNNNANNNGGCNCCTTTTNNNNNNNNNNNNNNNNNN
23	
24	

Figure 33

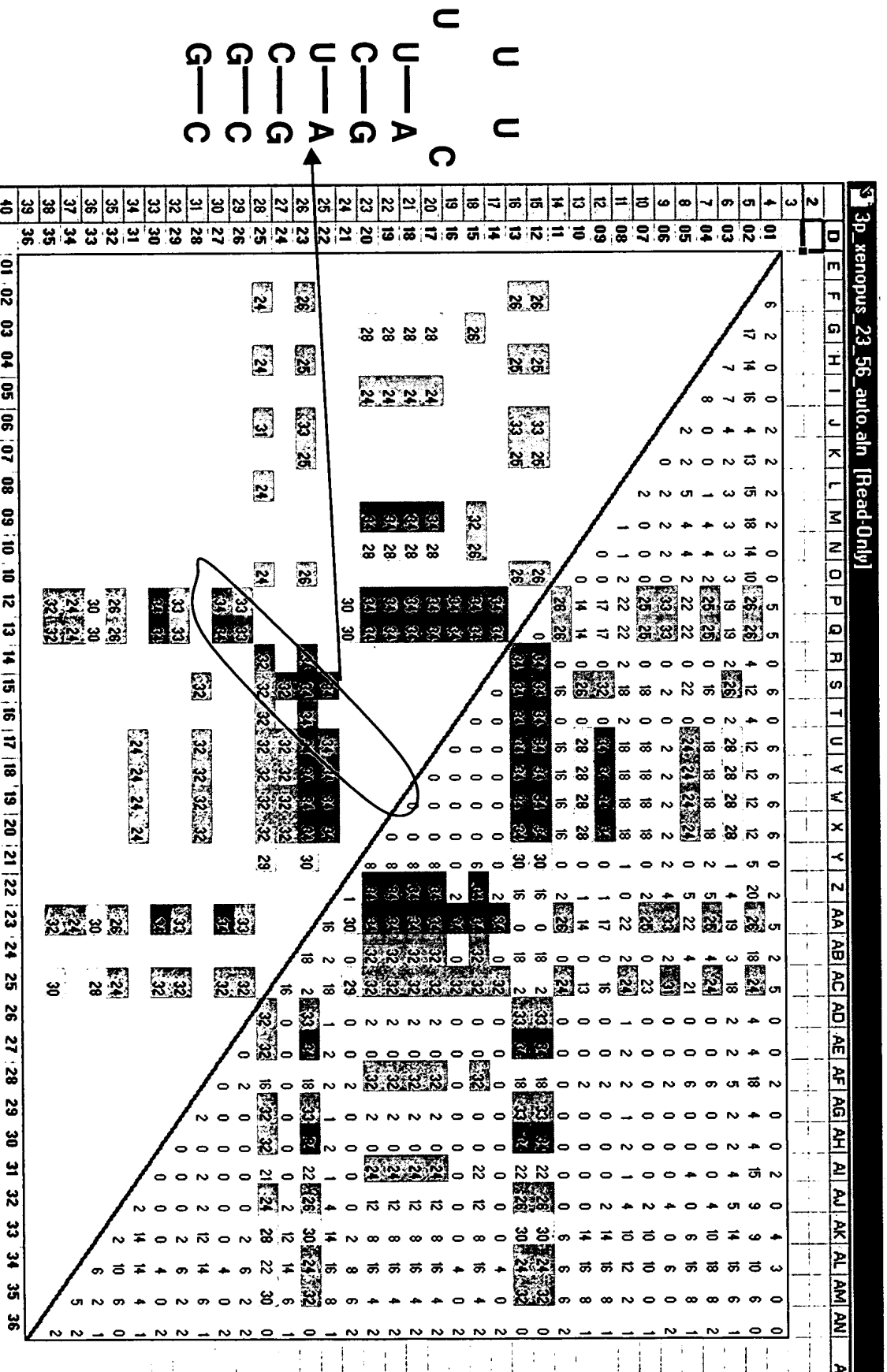


Figure 34

histone.domes (Read-Only)

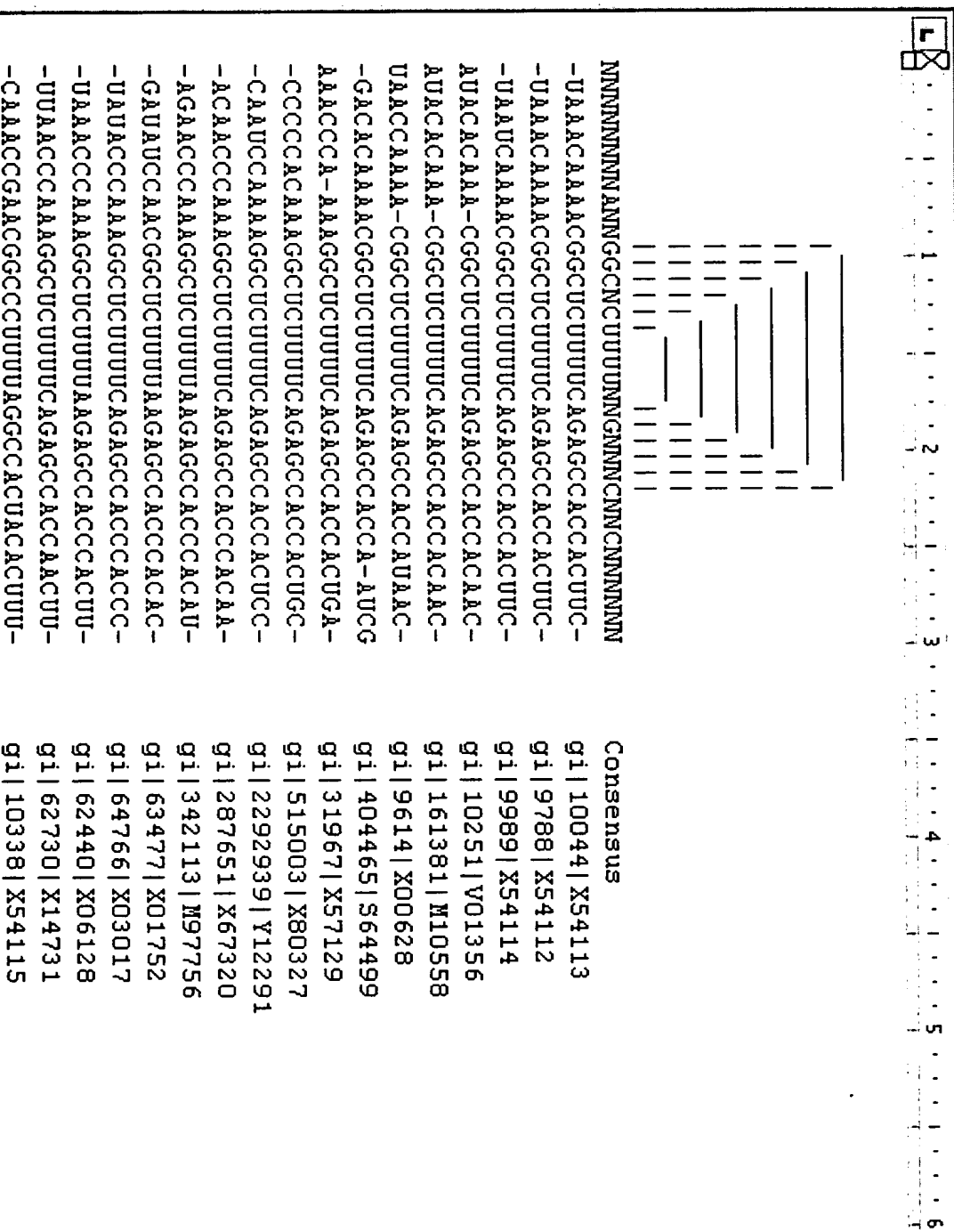


Figure 35

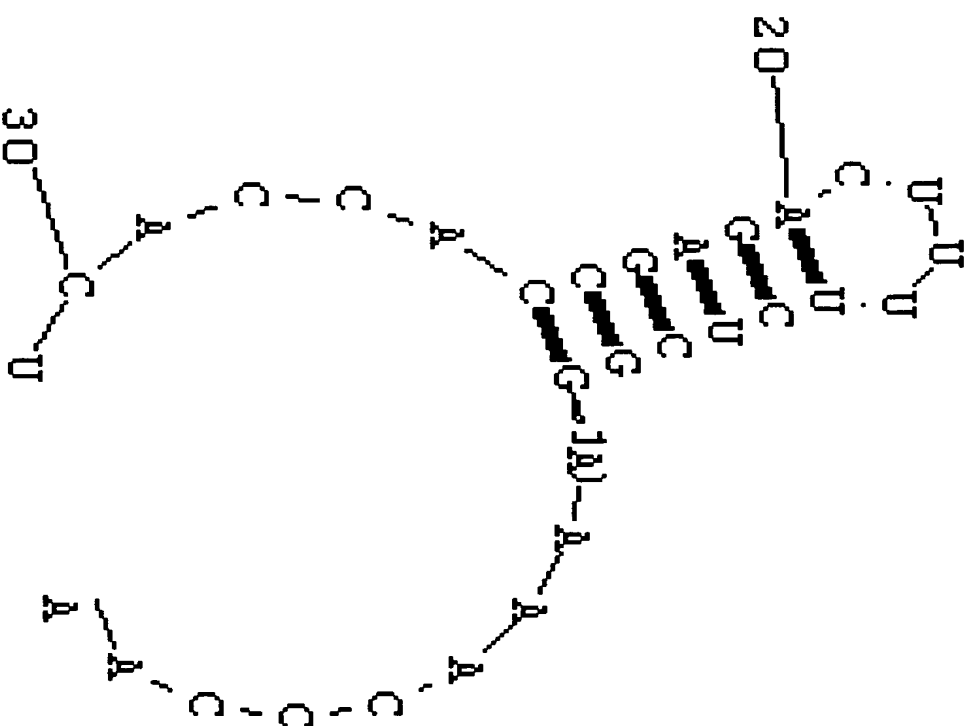


Figure 36

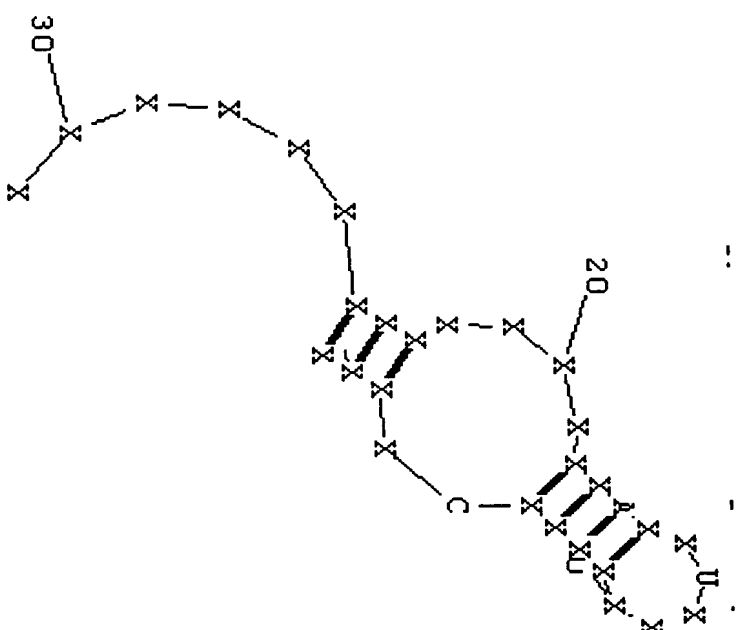


Figure 37

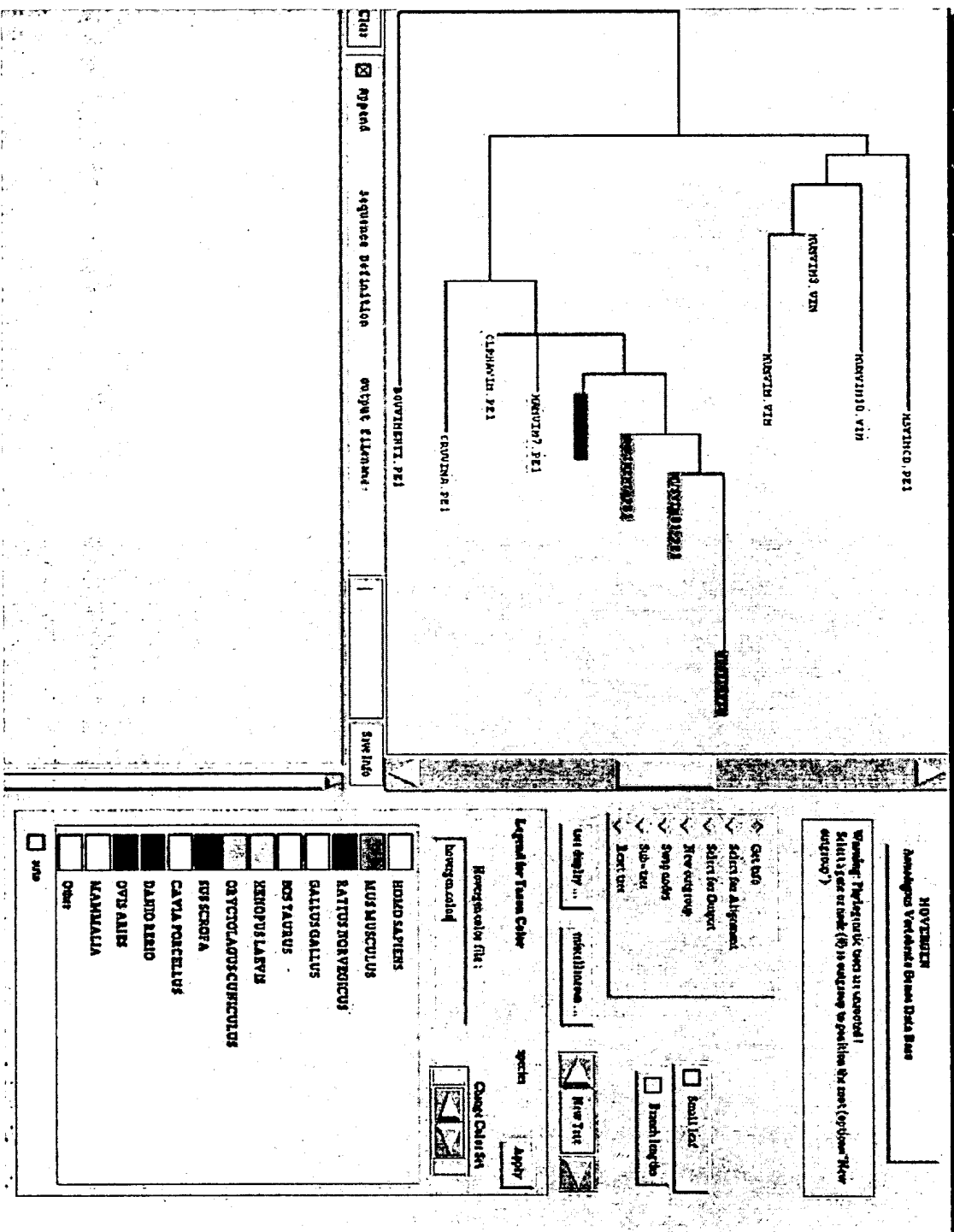


Figure 38

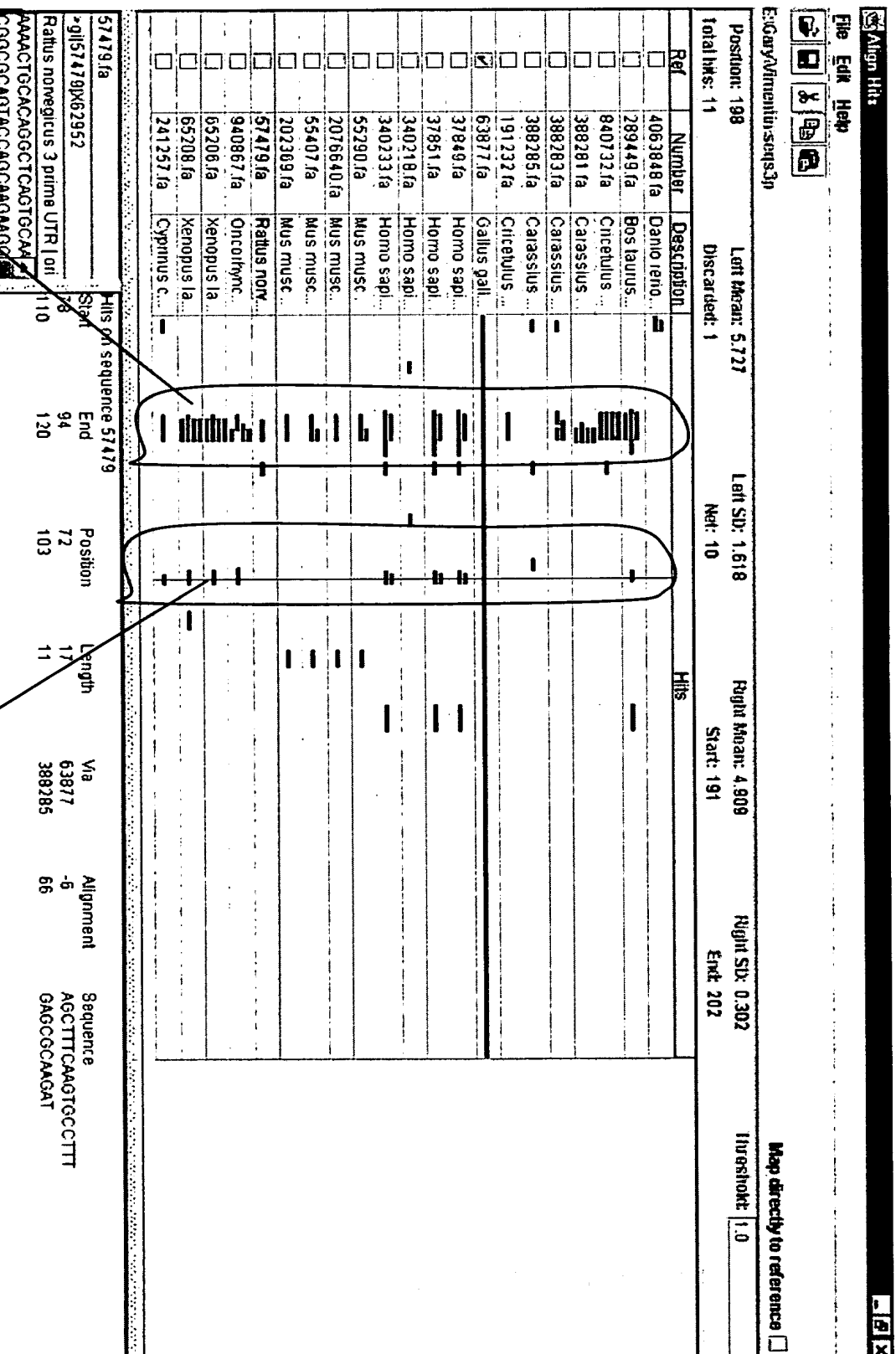


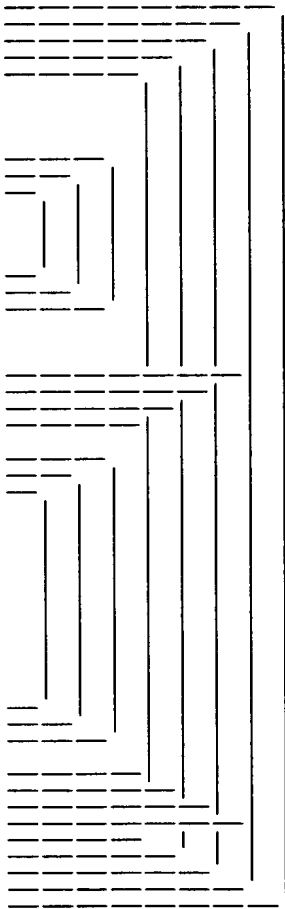
Figure 39

CLUSTAL W (1.74) multiple sequence alignment

```
gi|191232|M16718      TATCTTAAGGAAACAGCTTTTCAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGTAA
gi|202369|M26251      TATCTTAGGAAAACAGCTTTTCAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|2076640|Y07738     TATCTTAGGAAAACAGCTTTTCAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|289449|L13263      TATCTTAAGAAACAGCTTTTCAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|340233|M25246      TATCTTAAGAAACAGCTTTTCAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|37849|X56134       TATCTTAAGAAACAGCTTTTCAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|37851|Z19554       TATCTTAAGAAACAGCTTTTCAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|388281|L23840      CAACCCACAATTAACGTCTTCAAAAGTGCCCTTCTGCACAGAAATA--GCCTTGAGC
gi|388283|L23842      CTACCCACAATTAACGTCTTCAAAAGTGCCCTTCTGC-CAGAAGTACAAGCATTTGAGC
gi|55290|X51438       TATCTTAGGAAAACAGCTTTTCAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|55407|X56397       TATCTTAGGAAAACAGCTTTTCAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|57479|X62952       TATCTTAGGAAAACAGCTTTTCAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
gi|63877|V00447       TGTCTTAAGGAAGAGCTTTTCAAGTGCCCTTCTCCAGTTTTCATGAGCGCAAGATT
gi|65206|X16843       ACTTTGAAGAAAACAGCTTTTCAAGTGCCCTT-TGCAGTCAATGGAGAGCGCAAGATA
gi|65208|X16844       AATTGGAAGAAAACAGCTTTTCAAGTGCCCTT-TGCAGTTAATGGAGAGCGCAAGATA
gi|840732|X87227      TATCTTAAGGAAACAGCTTTTCAAGTGCCCTTCTGCAGTTTTCAGAGCGCAAGATA
```

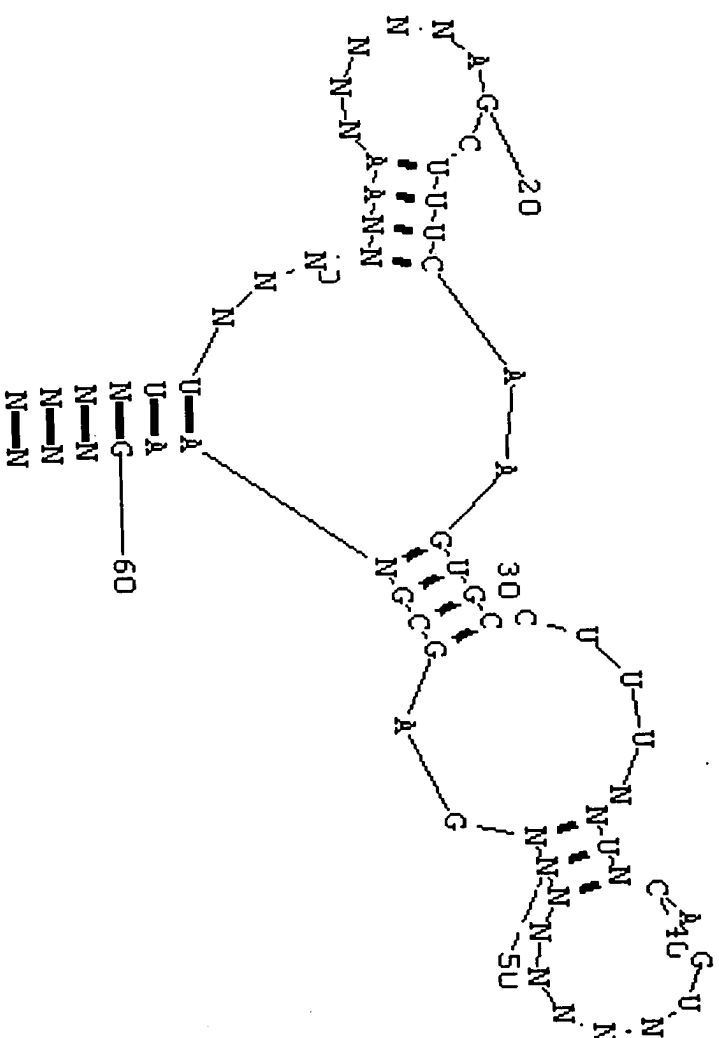
Figure 40

Score: 445.0



NNNNNNNNNNNAAANNNGCUUNNAAGUGCCUUNUNNCNNNNNNNNNNNNNGCANNNGNNN		Consensus	
UAUCUUAAGGAAACAGCUUUCAGUGCCUUUCUGCAGUUUUUCAGAGCGCAAGUAA	gi 191232 ML6718	gi 191232 ML6718	
UAUCUUAAGGAAACAGCUUUCAGUGCCUUUCUGCAGUUUUUCAGAGCGCAAGAUAA	gi 202369 M26251	gi 202369 M26251	
UAUCUUAAGGAAAAACAGCUUUCAGUGCCUUUCUGCAGUUUUUCAGAGCGCAAGAUAA	gi 2076640 Y07738	gi 2076640 Y07738	
UAUCUUAAGGAAAAACAGCUUUCAGUGCCUUUCUGCAGUUUUUCAGAGCGCAAGAUAA	gi 289449 L13263	gi 289449 L13263	
UAUCUUAAGGAAAAACAGCUUUCAGUGCCUUUCUGCAGUUUUUCAGAGCGCAAGAUAA	gi 340233 M25246	gi 340233 M25246	
UAUCUUAAGGAAAAACAGCUUUCAGUGCCUUUCUGCAGUUUUUCAGAGCGCAAGAUAA	gi 37849 X56134	gi 37849 X56134	
UAUCUUAAGGAAAAACAGCUUUCAGUGCCUUUCUGCAGUUUUUCAGAGCGCAAGAUAA	gi 37851 Z19554	gi 37851 Z19554	
UAUCUUAAGGAAAAACAGCUUUCAGUGCCUUUCUGCAGUUUUUCAGAGCGCAAGAUAA	gi 388281 L23840	gi 388281 L23840	
CAACCCACAUAACUGCUUCAAAGUGCCUUUCUGCAGCAAUA--GCUUUGAGC	gi 388283 L23842	gi 388283 L23842	
CUACCCACAUAACUGCUUCAAAGUGCCUUUCUGC-CAGAGUACAAGCAUUUGAGC	gi 55290 X51438	gi 55290 X51438	
UAUCUUAAGGAAAAACAGCUUUCAGUGCCUUUCUGCAGUUUUUCAGAGCGCAAGAUAA	gi 55407 X56397	gi 55407 X56397	
UAUCUUAAGGAAAAACAGCUUUCAGUGCCUUUCUGCAGUUUUUCAGAGCGCAAGAUAA	gi 57479 X62952	gi 57479 X62952	
UAUCUUAAGAAAAAAGCUUUCAGUGCCUUUCUGCAGUUUU-CAGGAGCGCAAGAUAA	gi 63877 V00447	gi 63877 V00447	
UGUCUUUAAAGGAAGACUUUCAAAGUGCCUUUCUGCAGUUUUUCAGAGCGCAAGAUUU	gi 65206 X16843	gi 65206 X16843	
ACUUUGAAGAAAAACAGCUUUCAGUGCCUUU-UGCAGUCAUUGGAGAGCGCAAGAUAA	gi 65208 X16844	gi 65208 X16844	
AAUUUGAAGAAAAACAGCUUUCAGUGCCUUU-UGCAGUUAUUGGAGAGCGCAAGAUAA	gi 840732 X87227	gi 840732 X87227	
UAUCUUAAGGAAAAACAGCUUUCAGUGCCUUUCUGCAGUUUUUCAGAGCGCAAGAUAA			

Figure 41



03708-05129

Figure 42

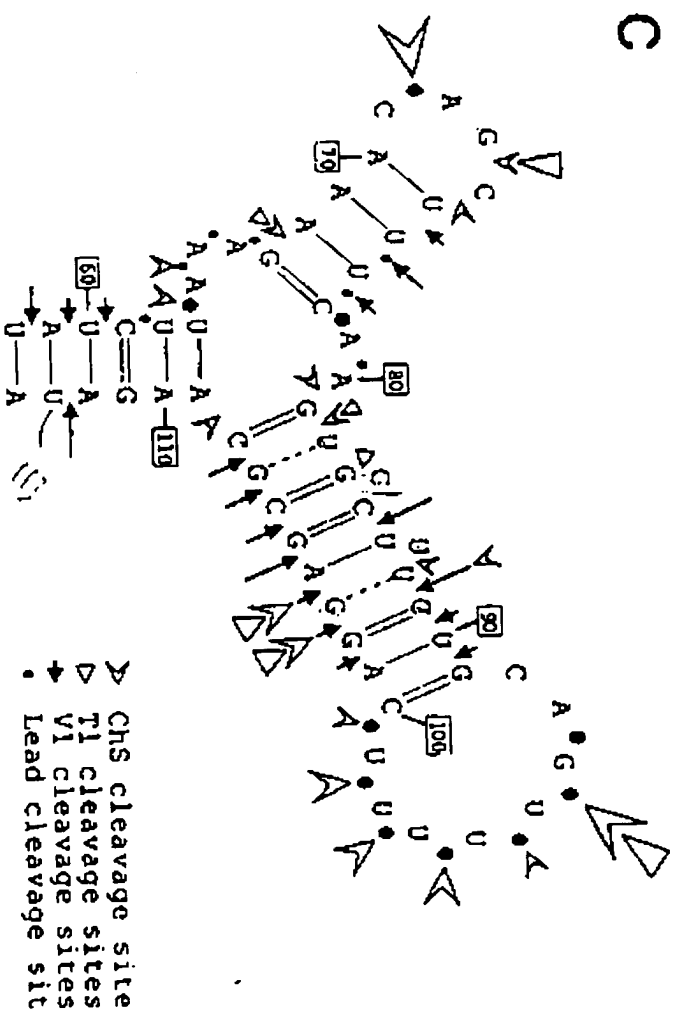


Figure 43

CLUSTAL W (1.74) multiple sequence alignment

```
qi|241257|S76850      ACCACGATGT-CTGTAGTTTACACTGTTGAA
qi|289449|L13263      TTTACAACATAATCTAGTTTACCGAAGACGC
qi|340233|M25246      TTTACAACATAATCTAGTTTACAGAAAAATC
qi|37849|X56134       TTTACAACATAATCTAGTTTACAGAAAAATC
qi|37851|Z19554       TTTACAACATAATCTAGTTTACAGAAAAATC
qi|388285|L23841      TCCACACTGGAGTAAAACGAGGAAGAAATGAA
qi|63877|V00447       TTTACAATGGAGTCTAGTTTACAAATAGCAA
qi|65206|X16843       GCTTCCTTCT-GTCTAGTTTACAGACTGTAA
qi|65208|X16844       GCTTCCTTCT-GTCTAGTTTACAGACTATGT
qi|940867|Z50738      ACCACACTGA-GTCTAGTTTACACTTGCCT
```

Figure 44

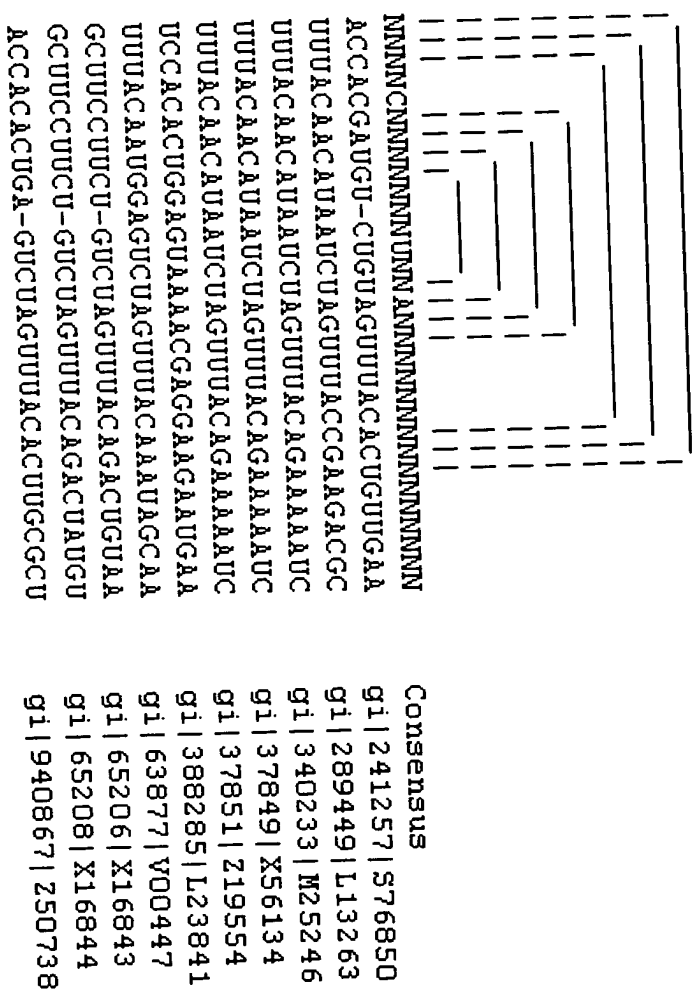
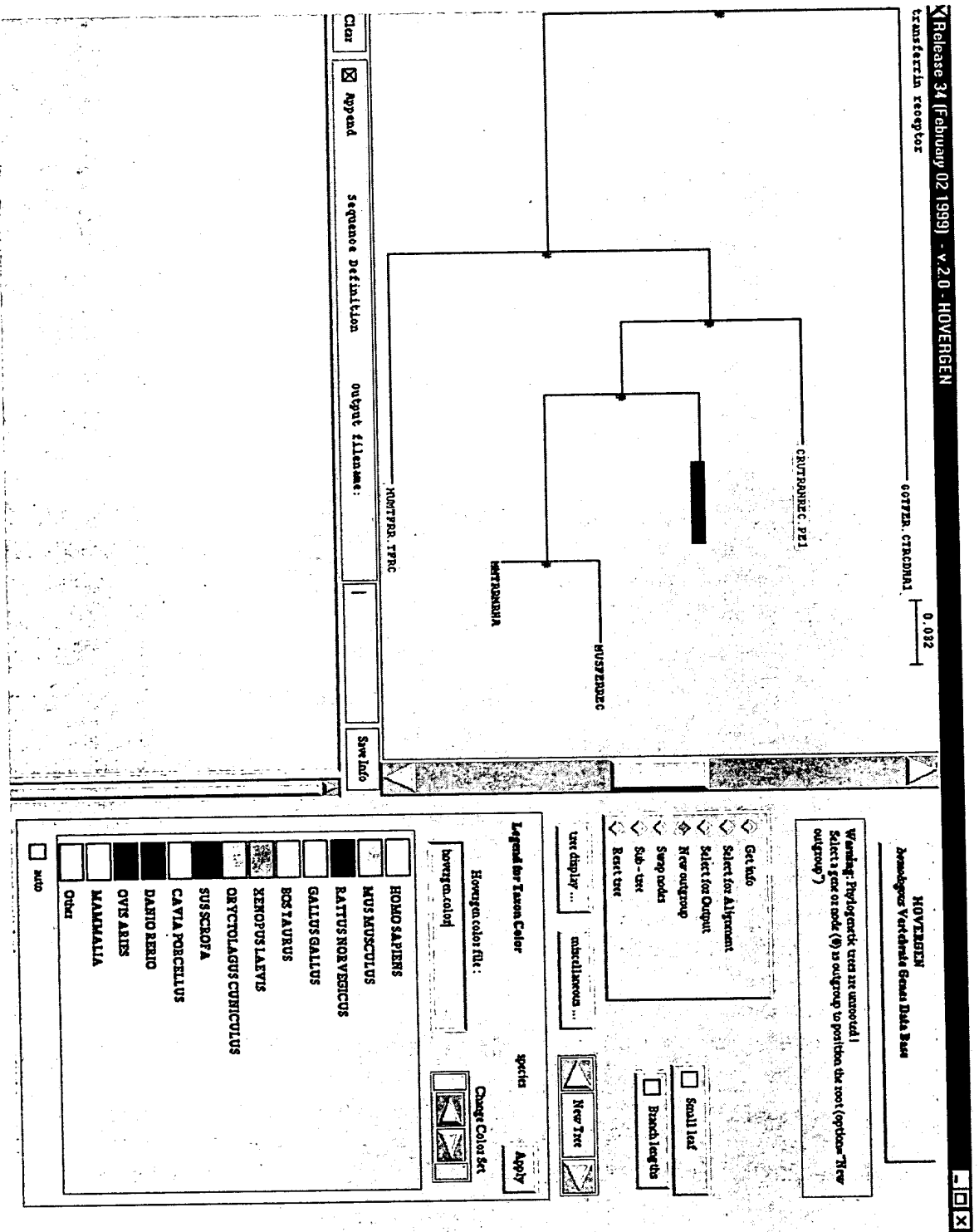
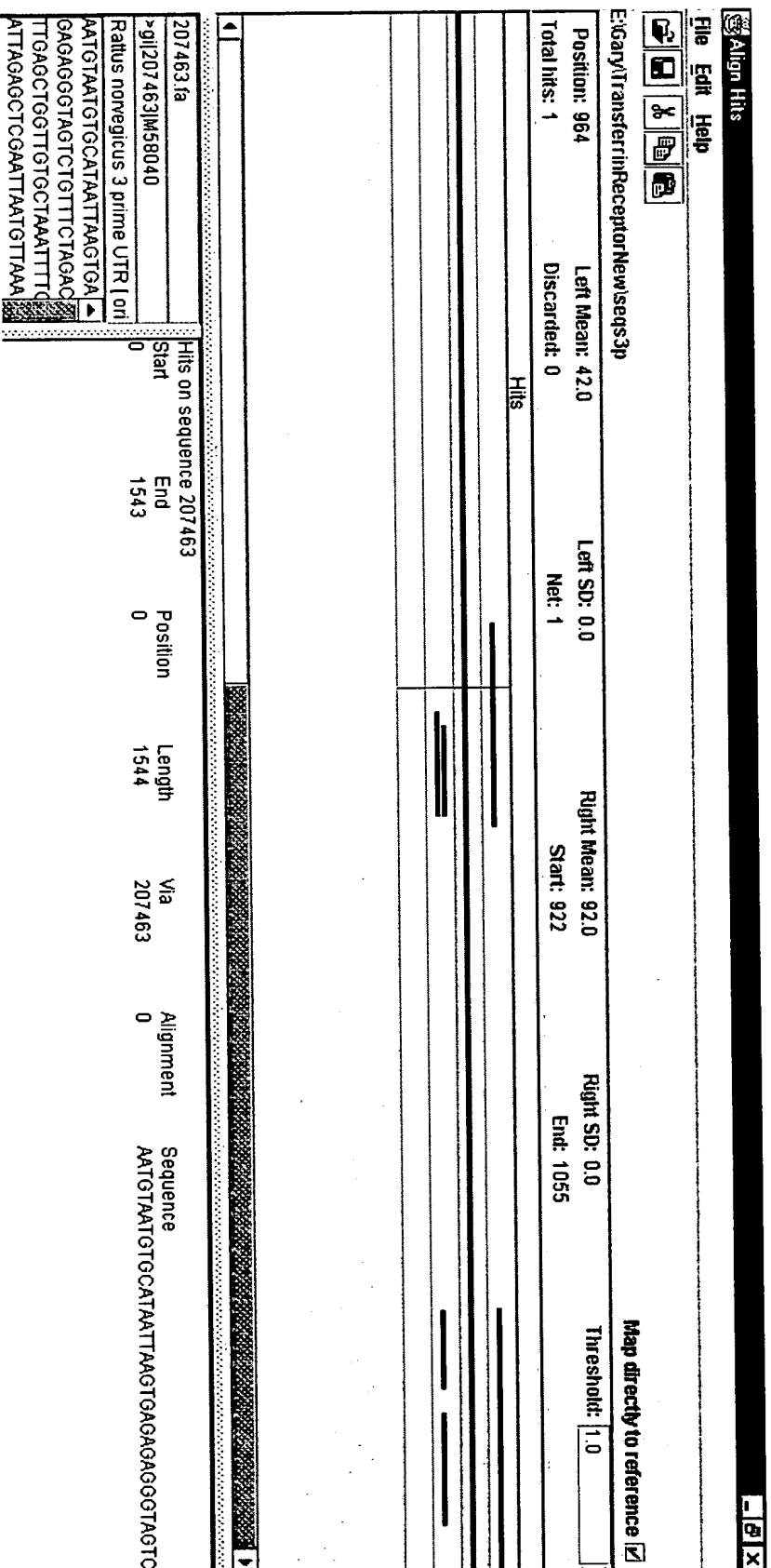


Figure 45



0931063-051 [UNITED STATES]

Figure 46



09310667.051299

Figure 47

CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040
GTTTTGGCAGTGAATATTTATGTTTATTTATCAGTGACAGAGTTCACTATAAATAGTGTGTTTTTAAT
gi|37432|X01060
CCTTTGGCAGTGAATATTTATGTTTATTTATCAGTGACAGAGTTCACTATAAATGGTGTGTTTTTAAT
gi|63357|X13753      -----
TGAGATATTTATTTTATTTATTCAGTGACAGCGTTCACCTATAAATGGTGTGTTTTTAAT
```

09310667.051299

Figure 48

Score: 102.0

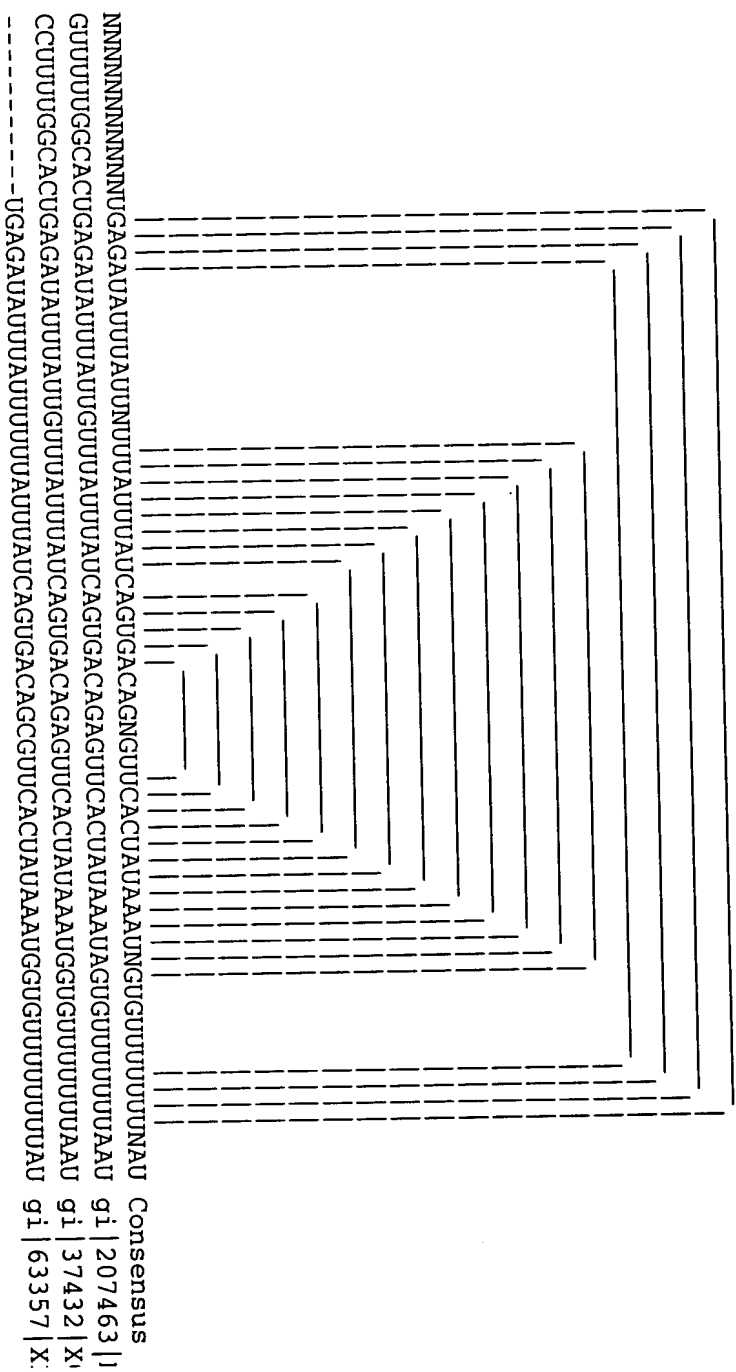
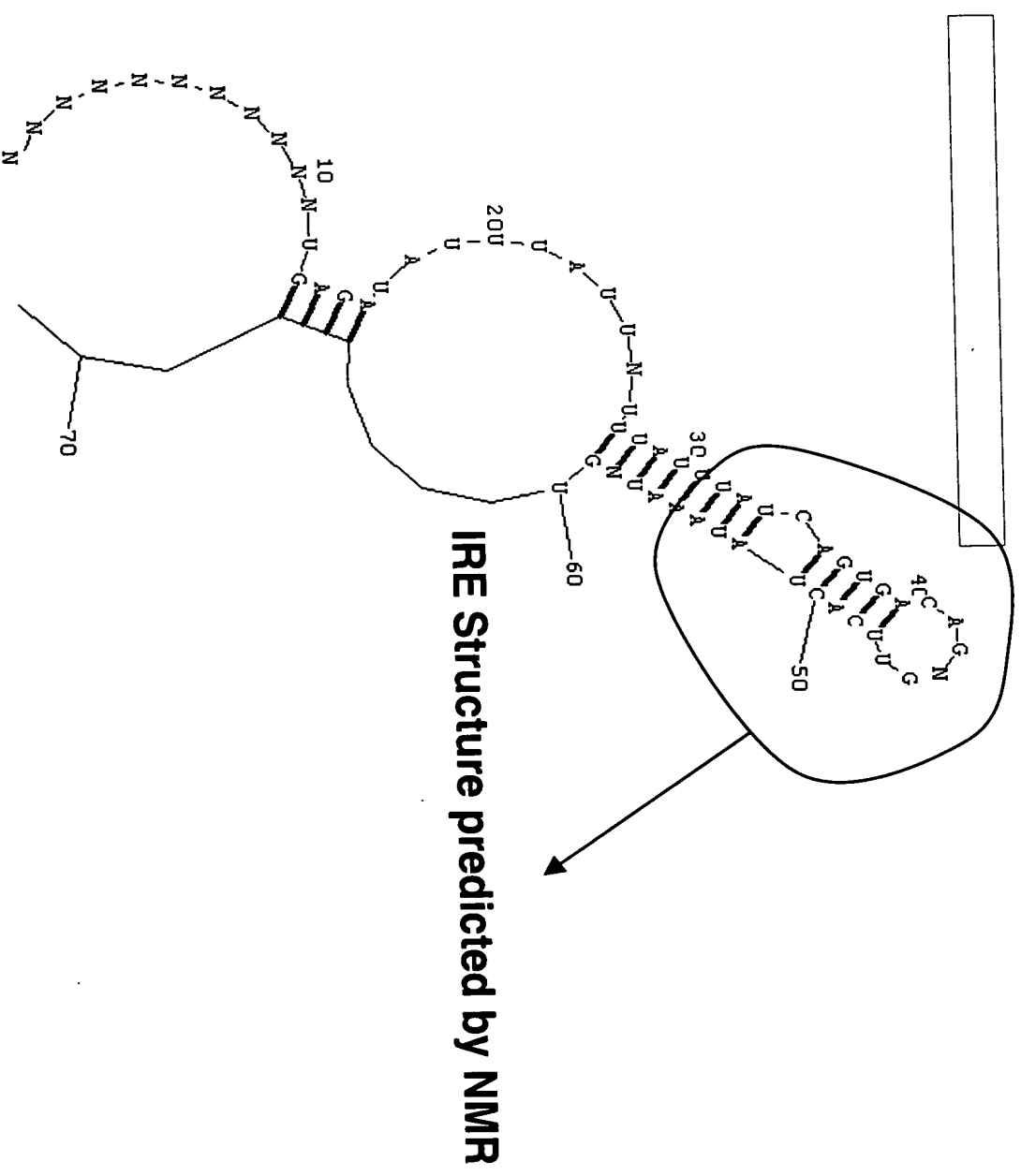


Figure 49



09310667-051299

Figure 50

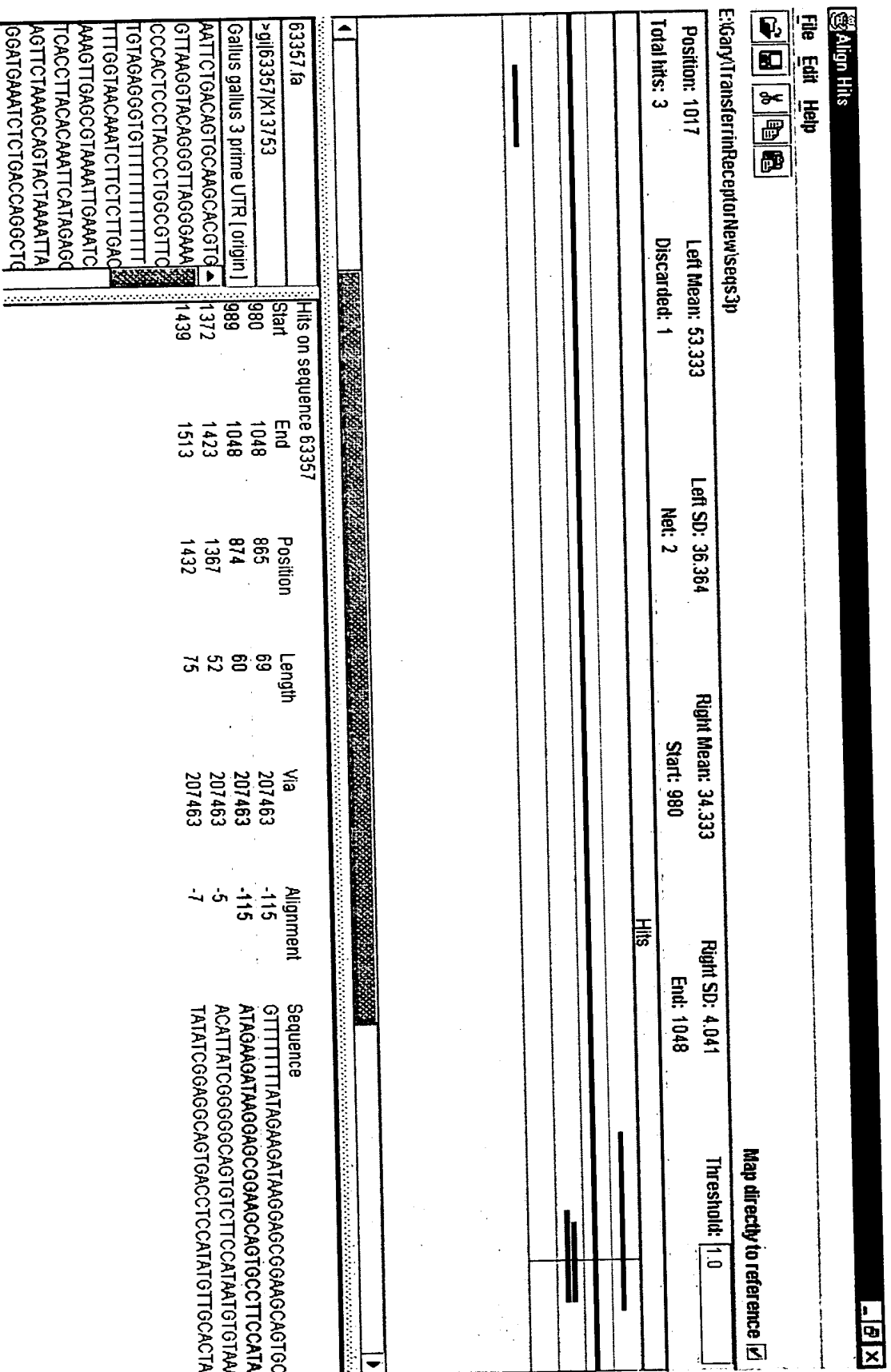


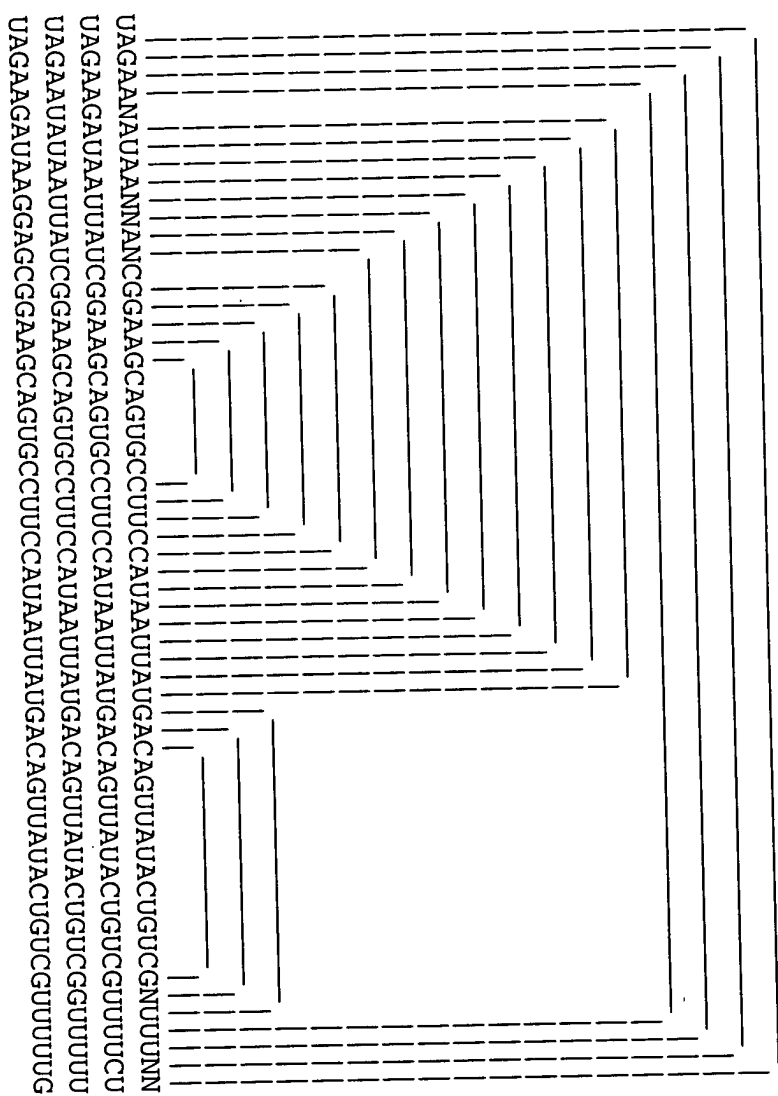
Figure 51

CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040
TAGAAGATAATTATCGGAGCAGTGCCCTTCATAATTATGACAGTTACTGTCGTTTCT
gi|37432|X01060
TAGAATATAATTATCGGAGCAGTGCCCTTCATAATTATGACAGTTACTGTCGTTTTT
gi|63357|X13753
TAGAAGATAAGAGCGGAGCAGTGCCCTTCATAATTATGACAGTTACTGTCGTTTTG
```

Figure 52

Score: 115.0



Consensus
gi | 207463 | M58040
gi | 37432 | X01060
gi | 63357 | X13753

Figure 53

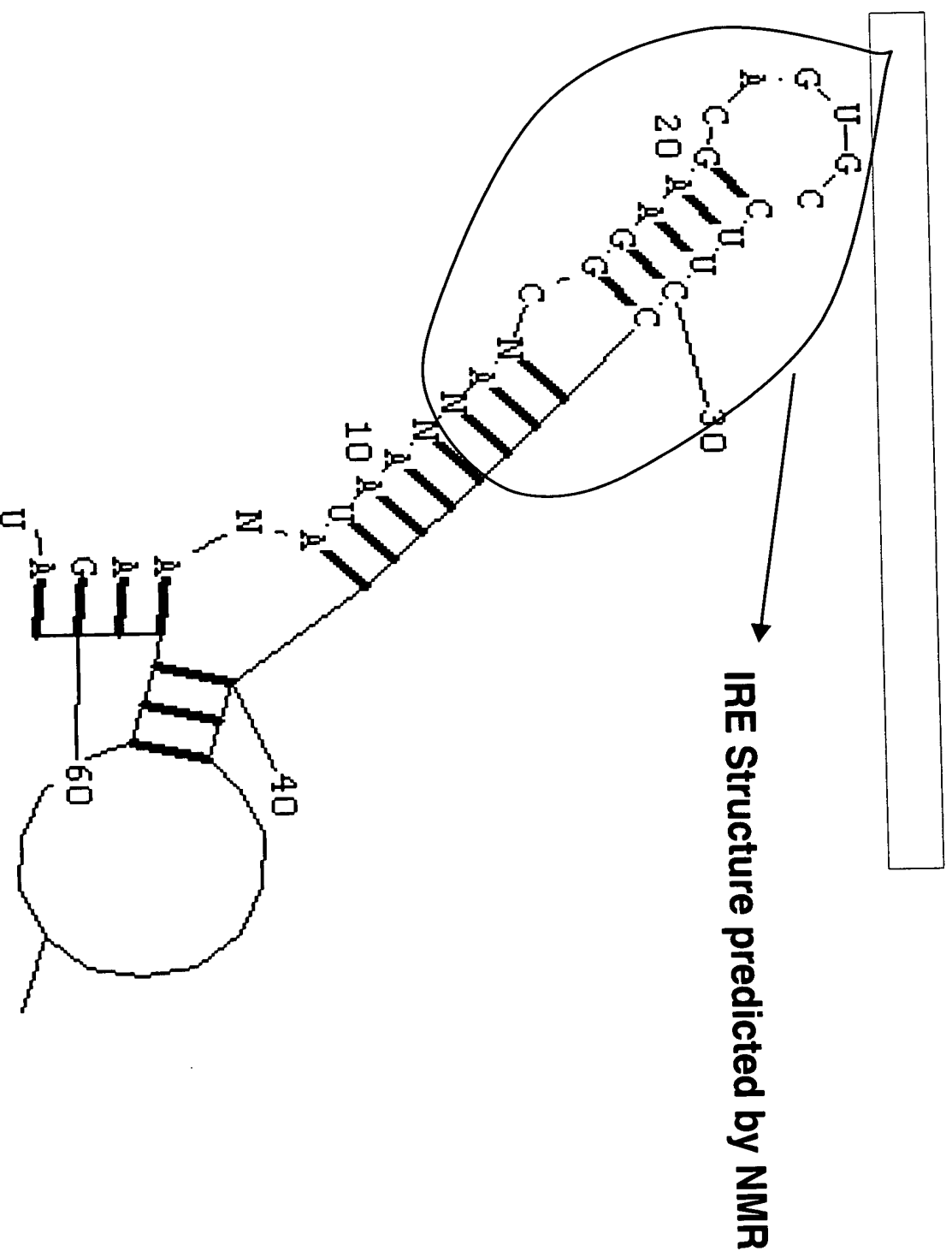
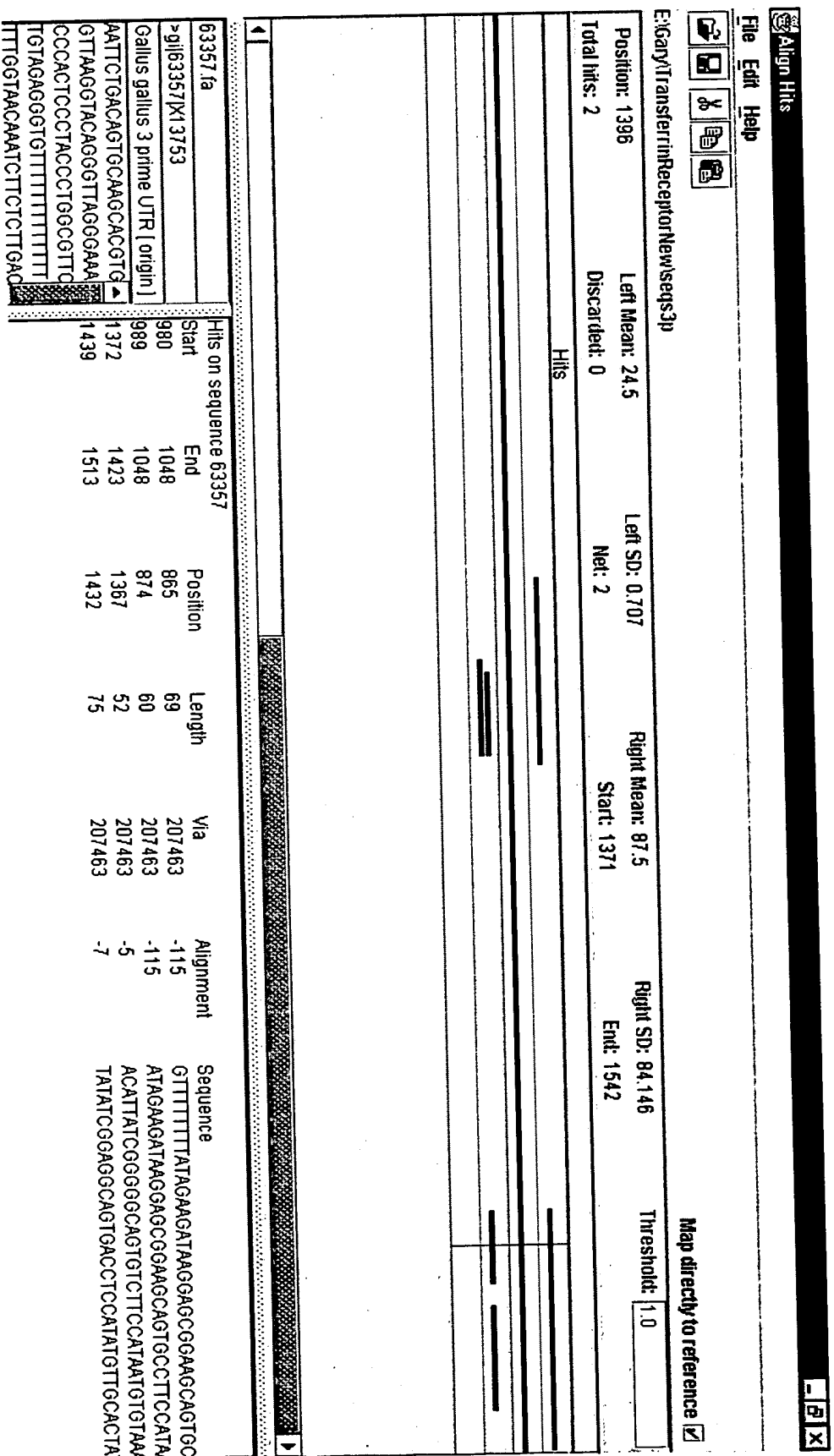


Figure 54



09310657.051299

Figure 55

CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040      ACATTATCGGGAGCAGTGTCTTCCATAATGTATAAAGACAAGGTAGTTTTT
gi|37432|X01060      ACATTATCGGGAGCAGTGTCTTCCATAATGTATAAAGACAAGGTAGTTTTT
gi|63357|X13753      ACATTATCGGGGCAGTGTCTTCCATAATGTATAAAGACAAGGTAGTTTTT
*****
```

Figure 56

Score: 108.0

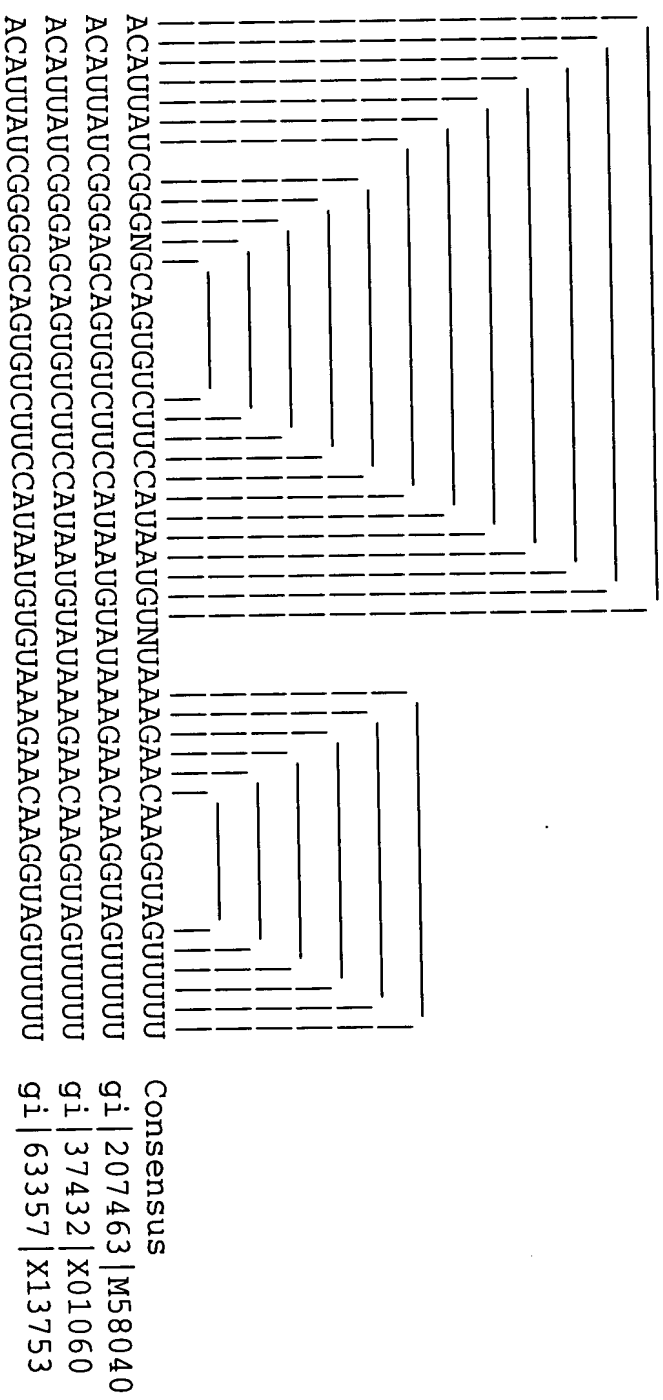
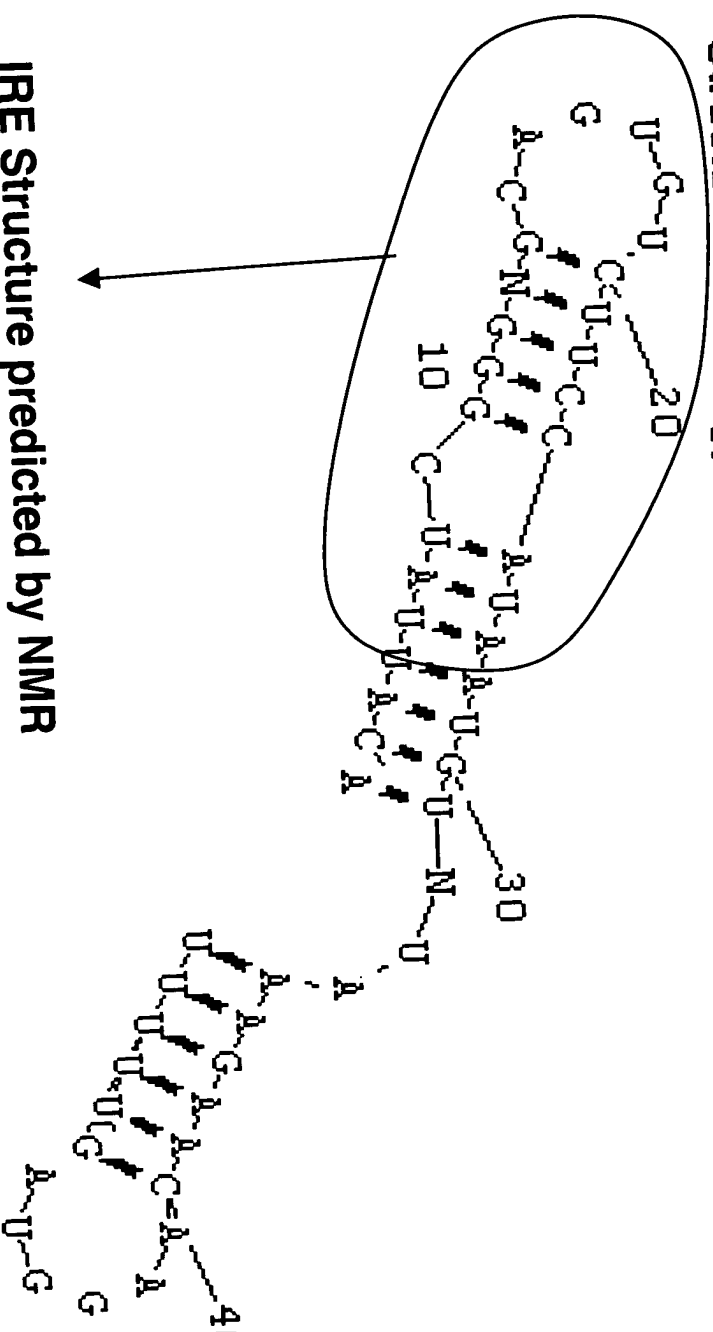


Figure 57

Structure: 1 Energy = 108.0 nothing to say !



09310667.051299

Figure 58

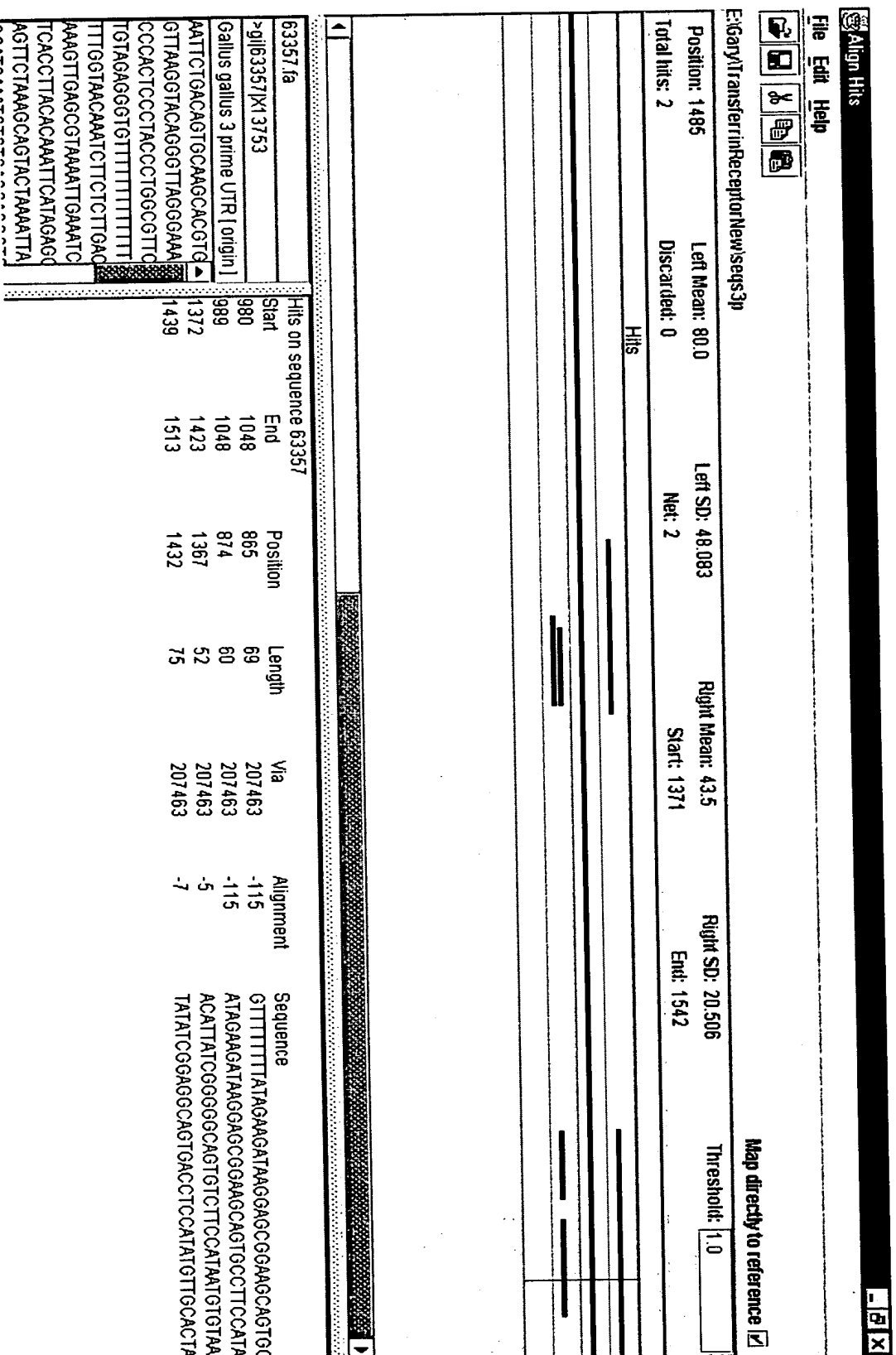


Figure 59

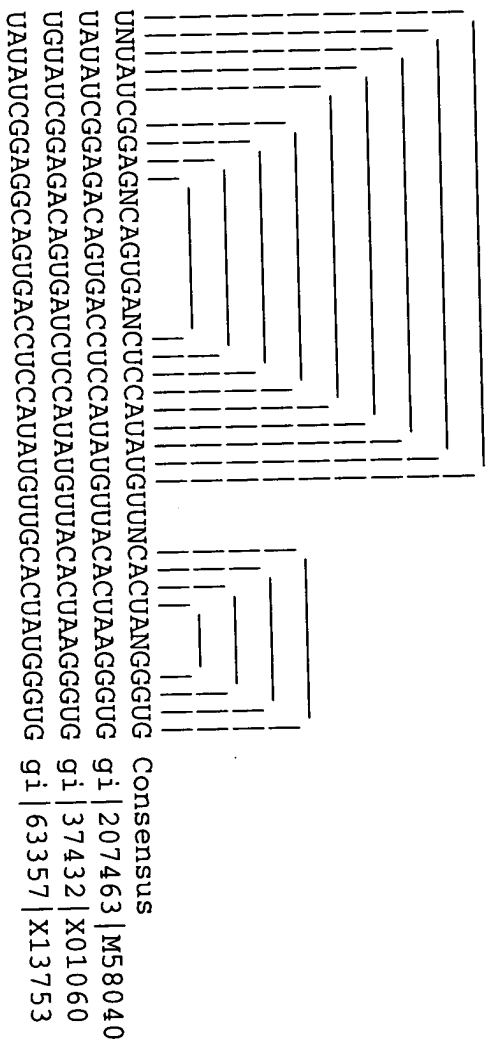
CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040      TATATCGAGACAGTGACCTCCATATGTGTACACTAAGGCTG
gi|37432|X01060      TGTATCGAGACAGTGATCTCCATATGTGTACACTAAGGCTG
gi|63357|X13753      TATATCGAGGCGAGTGACCTCCATATGTGTGCACTATGGGTG
* * * * *
* * * * *
```

09310657.051299

Figure 60

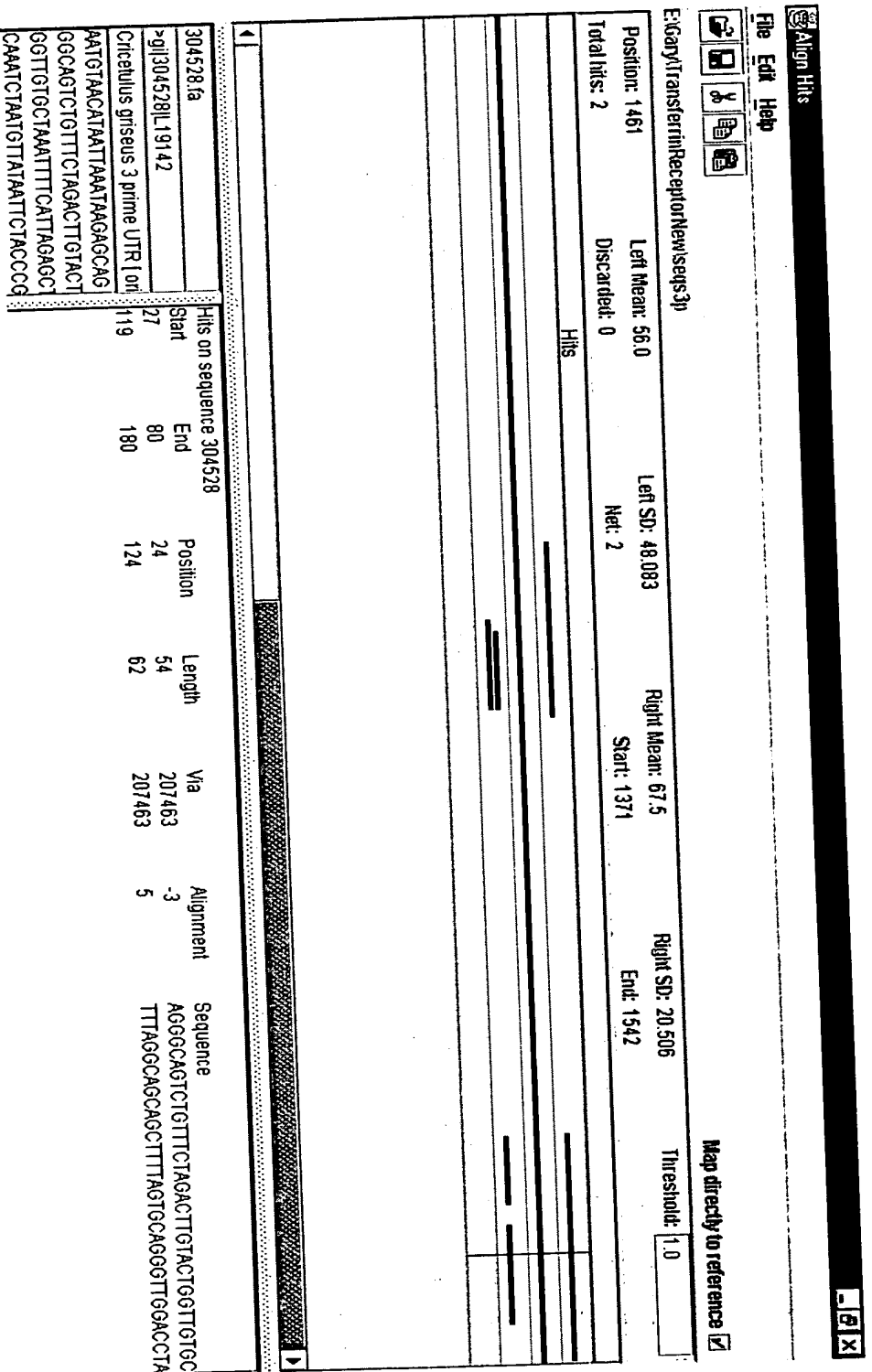
Score: 78.0



IRE Structure predicted by NMR

03090100

Figure 62



09310567.051299

Figure 63

CLUSTAL W (1.74) multiple sequence alignment

```
gi|207463|M58040      GTACGTAATTATCGGGACAGTGTTCCCATAATTTCTTCATGCGATGACATCTT
gi|37432|X01060      GTAAGTAATTATCGGGACAGTGTTCCCATAATTTCTTCATGCAATGACATCTT
gi|63357|X13753      GTACGTAATTATCGGGACAGTGTTCCCATAATTGTTTTCATGAAATGTCATCTG
```

09310667.051299

Figure 64

Score: 84.0

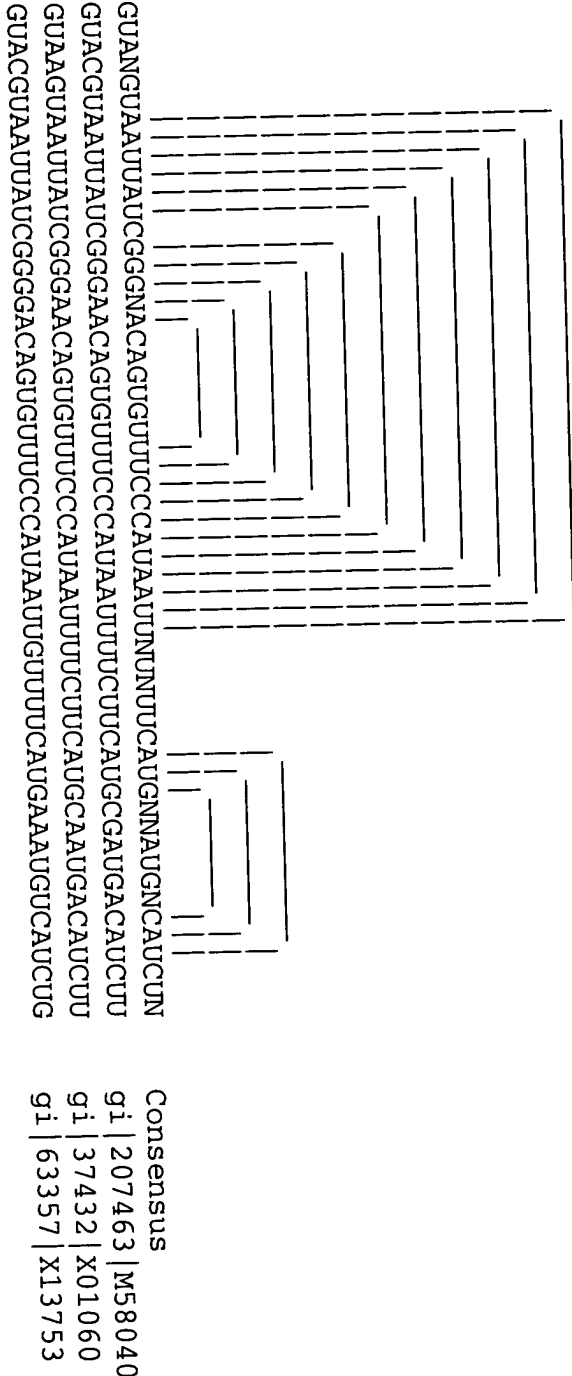


Figure 65

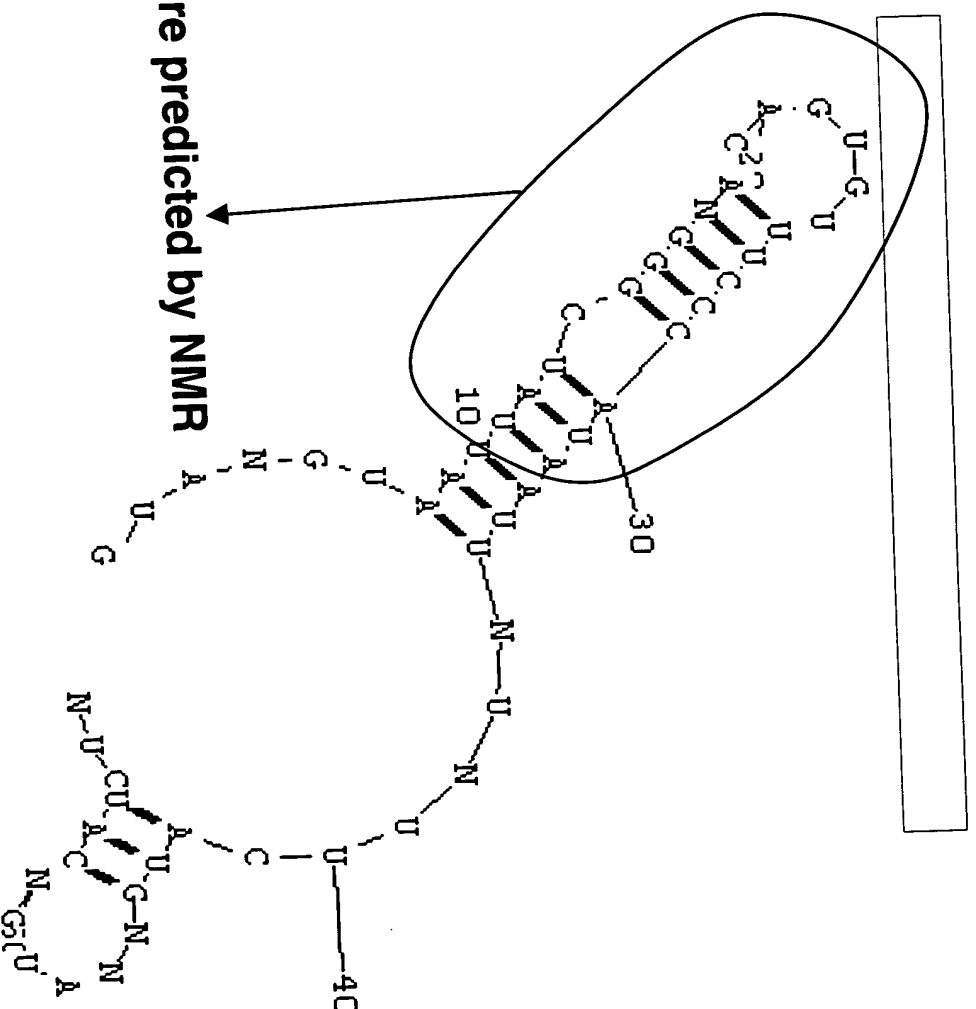


Figure 66

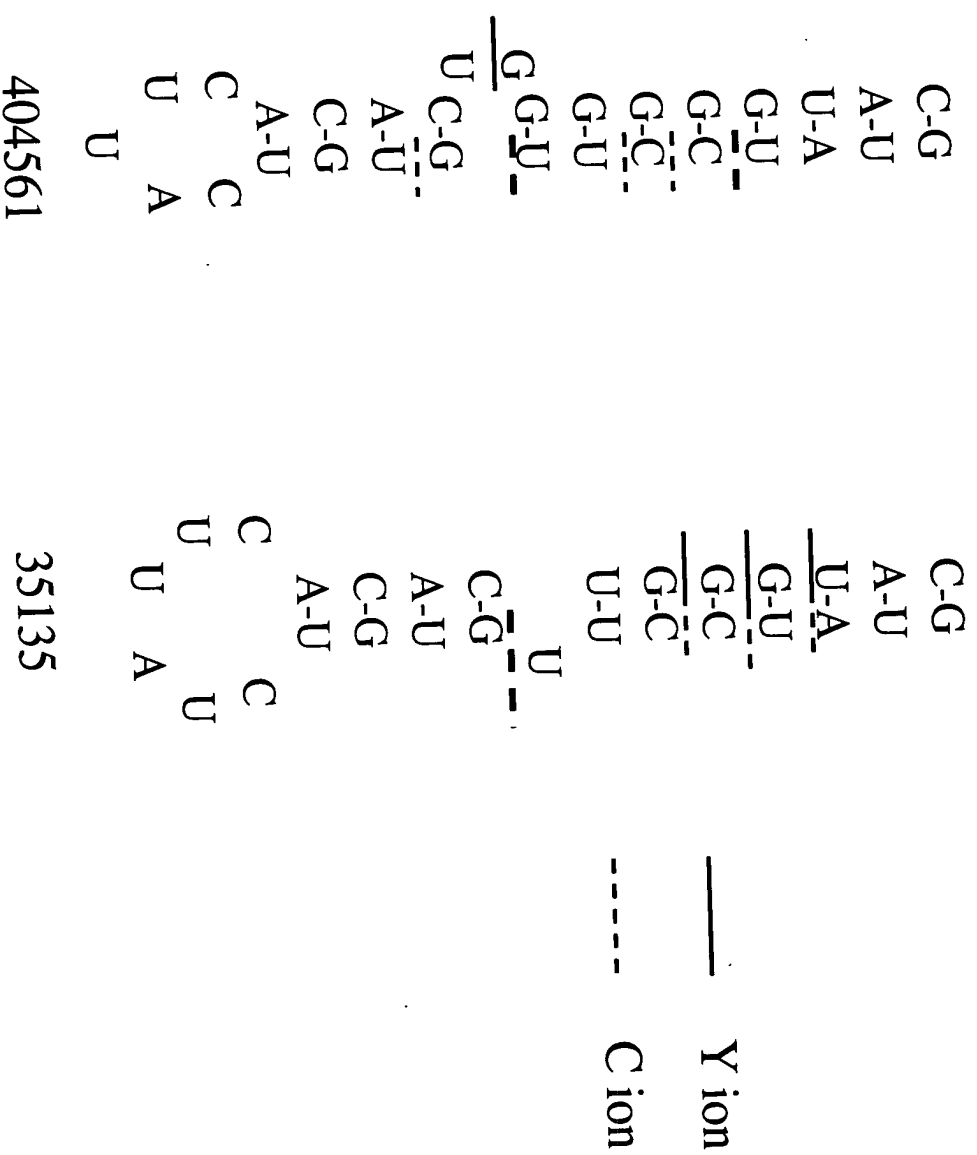


Figure 67

A	
1	CLUSTAL W (1.74) multiple sequence alignment
2	
3	
4	gi 163448 M92441 -ACTGGGAGATGGG--TCACACTTATCTGTGTTCCCTATGGAACCTATTGAATAT----
5	gi 163448 M92441b ---TGGGAGATGGG--TCACACTTATCTGTGTTCCCTATGGAACCTATTGAATATTT--
6	gi 200123 M87223 -CTAGAAGATGGGG--TCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAATATTTGT
7	gi 200123 M87223b ---TAGAAGATGGGG--TCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAATATTTGT
8	gi 205807 J04791 --CTAGGAGATGGGG--TCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAATATTTTA
9	gi 205807 J04791b ---TAGGAGATGGGG--TCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAATATTTGT
10	gi 35135 X55362 ---CTAGGATATGGG--TCACACTTATCTGTGTTCCCTATGGAACCT--TTGAATATTTGT
11	gi 404561 S64539 ----ACGAGATGGGGGTCACACTTA-CTGTGTTCCCTATGGAACCT--TTGAATATTTG-
12	gi 404561 S64539b ---TAGGAGATGGGGGTCACACTTA-CTGTGTTCCCTATGGAACCTATTGGAATATTG--
13	gi 63712 X64710 --CTAGGAGATGGG--TCACATTTATCTGTGTTCCCTATGGAACCTATTGGAATATTG----
14	gi 63712 X64710b GACTAGGAGATGGG--TCACATTTATCTGTGTTCCCTATGGAACCTATTGGAATATTG----
15	gi 64953 X56316 -ACTGCGAGATGGG--TCACA--TATCTGTGTTCCCTATGGAACCTTTTTTTTC--
16	* **** * **** ** *****
17	NNNNNNANATGGGNNNTCACANNNTANCTGTGTTCCCTATGGAACCTNNNTNNNTNNNN
18	

Figure 68

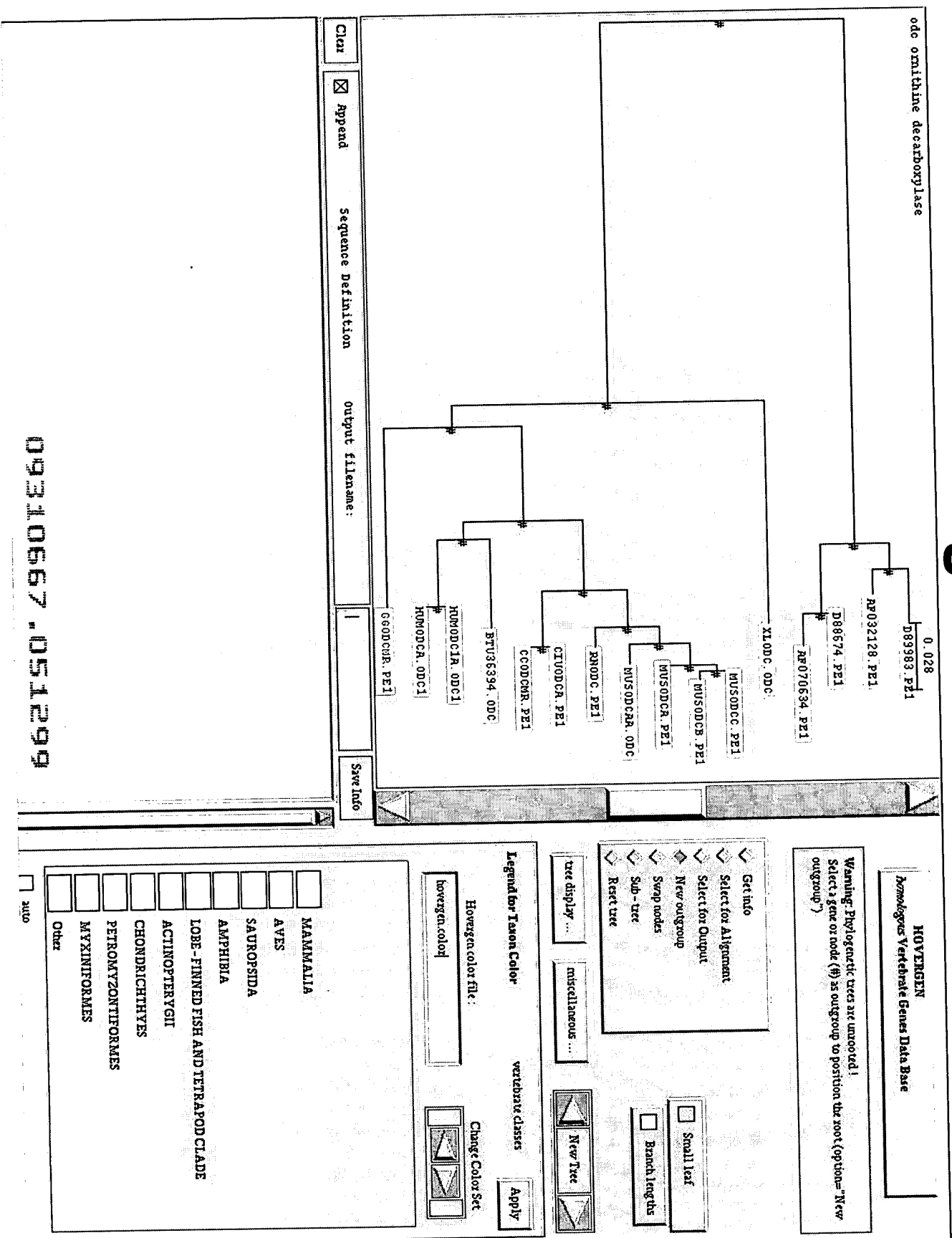


Figure 69

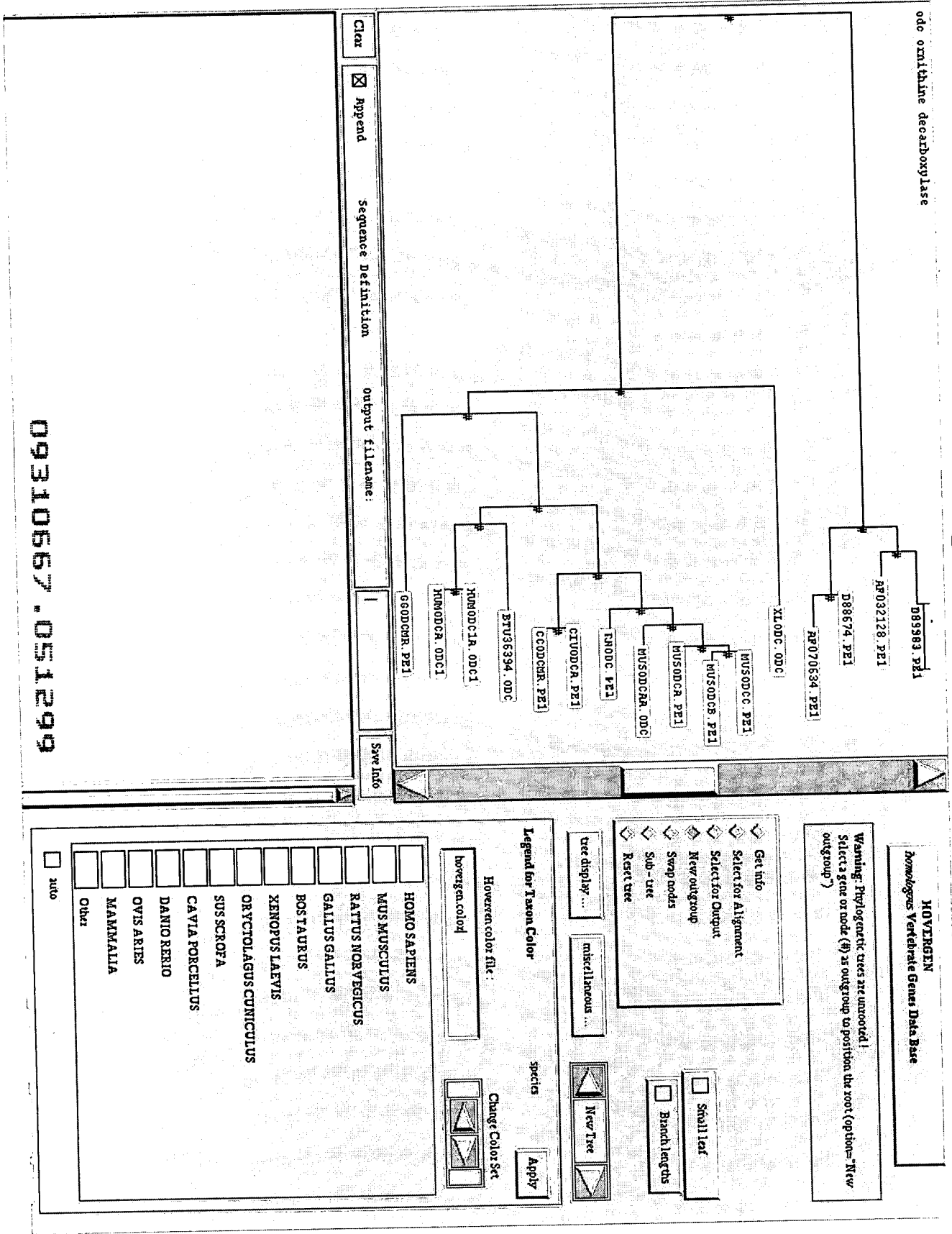


Figure 70

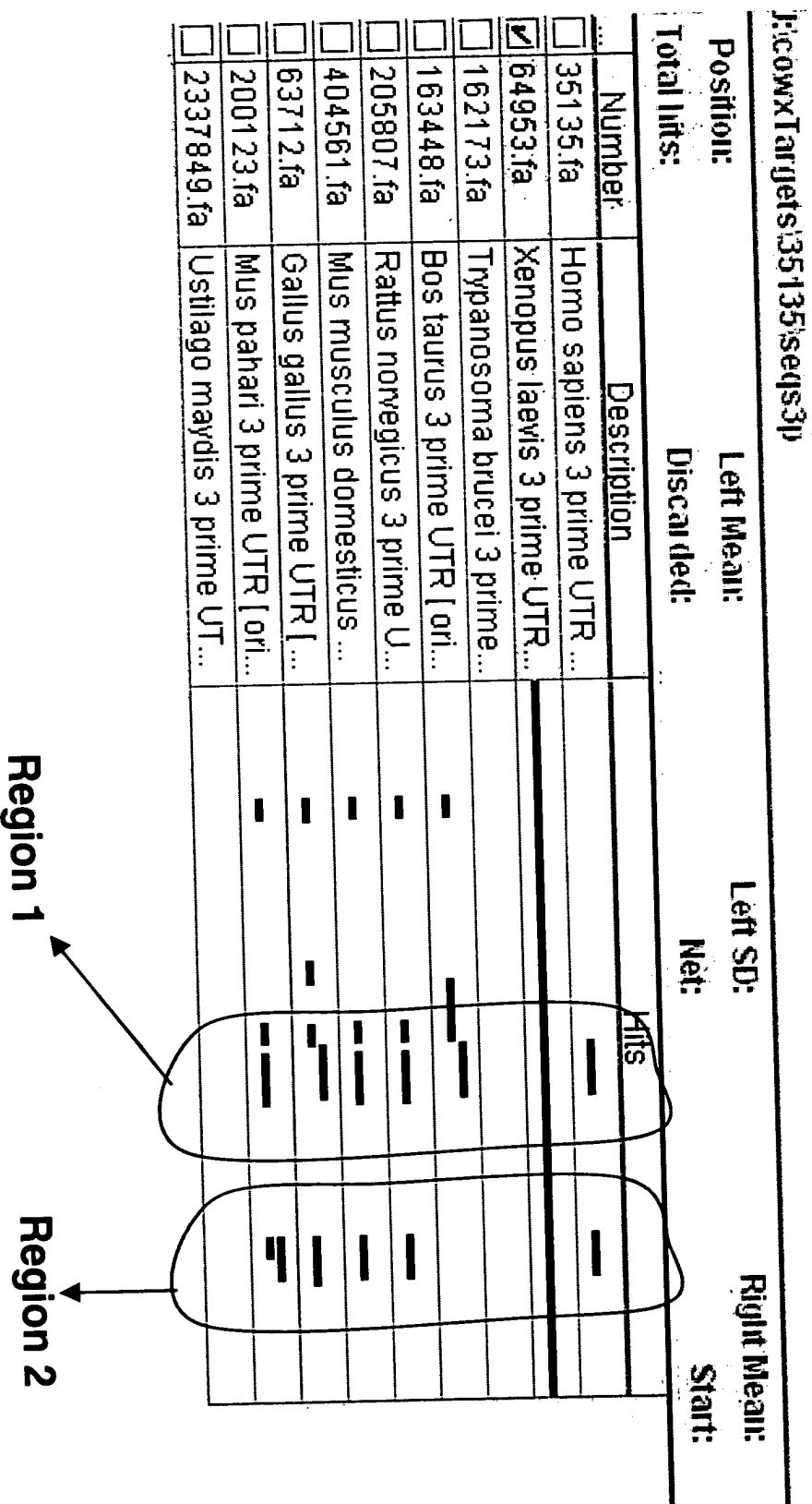
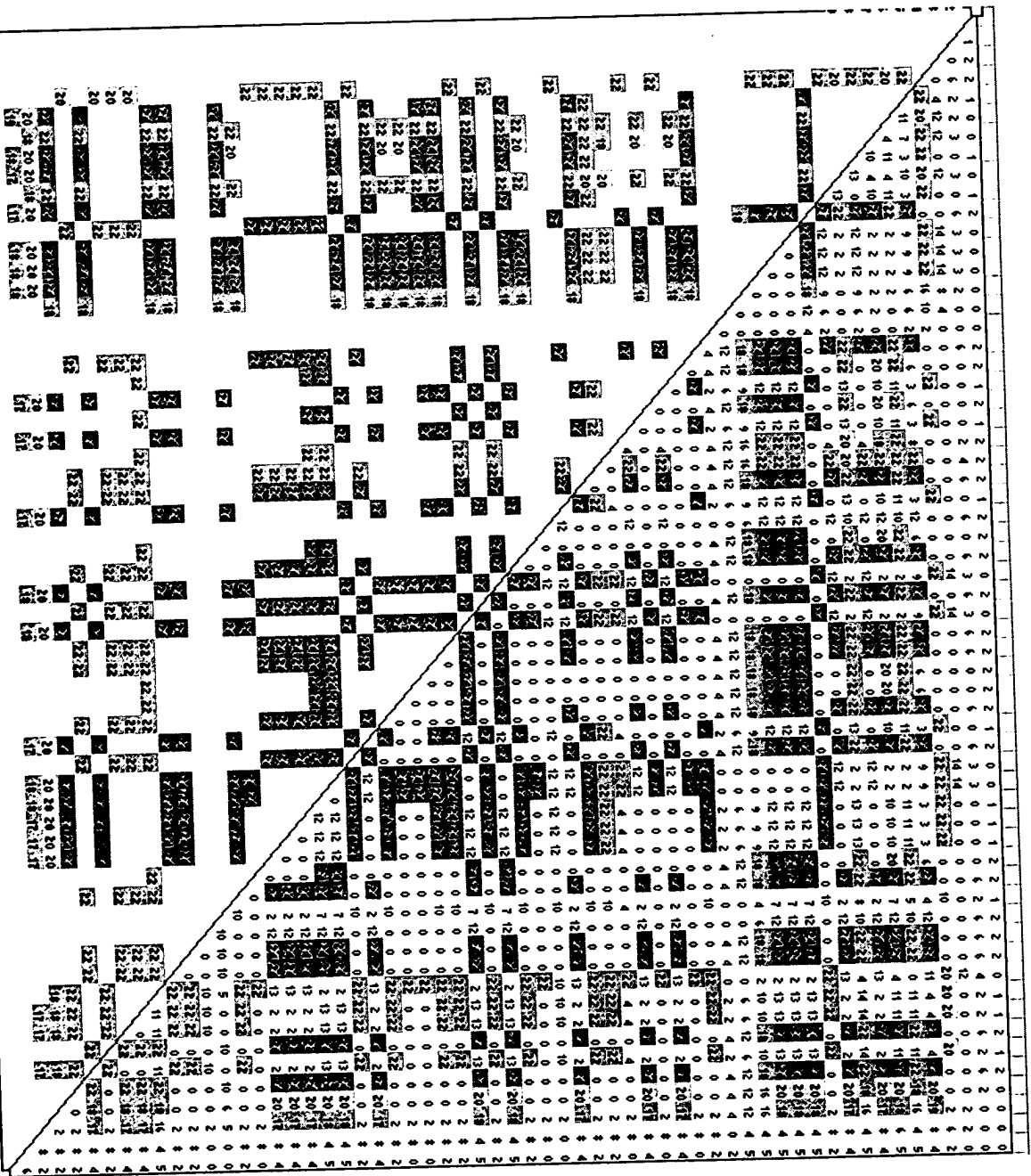
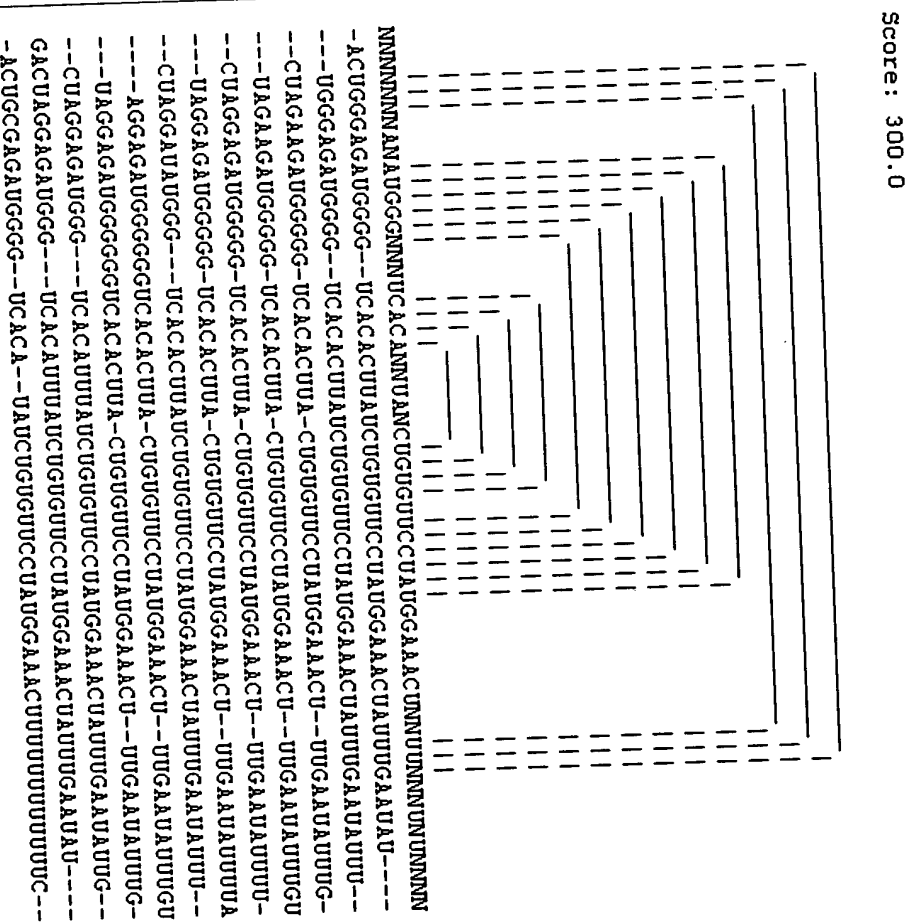


Figure 71



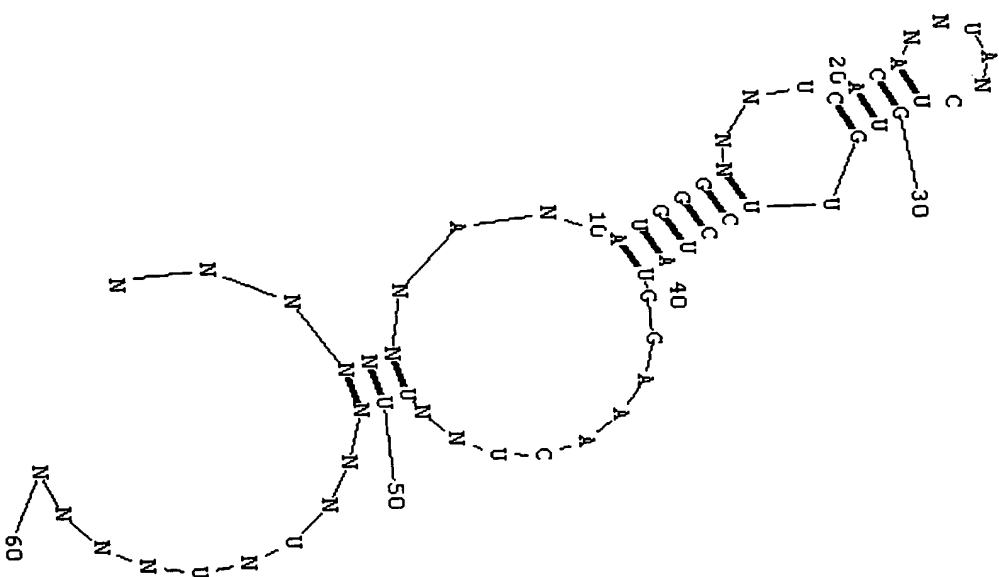
09310667-051299

Figure 72



Consensus
gi|163448|M92441
gi|163448|M92441b
gi|200123|M87223
gi|200123|M87223b
gi|205807|J04791
gi|205807|J04791b
gi|35135|X55362
gi|404561|S64539
gi|404561|S64539b
gi|63712|X64710
gi|63712|X64710b
gi|64953|X56316

Figure 73



09310667-051299

Figure 74

CLUSTAL W (1.74) multiple sequence alignment

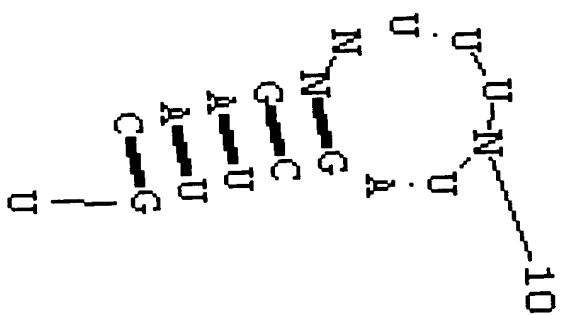
```
gi|404561|S64539      CAAACGTTTGTAGCTTGT
gi|63712|X64710      CAAGTATTGTAGCTTGT
gi|64953|X56316      CAAGCATTGTAGCTTGT
gi|35135|X55362      CAAGCATTGTAGCTTGT
gi|200123|M87223      CAAGCATTGTAGCTTGT
gi|205807|J04791      CAAGCATTGTAGCTTGT
*****
```

Figure 75

Score: 60.0

CAAGNMUUUUUAGCUUGU	Consensus
CAAGCGUUUGUAGCUUGU	gi 404561 S64539
CAAGUAUUUUGUAGCUUGU	gi 63712 X64710
CAAGCAUUUUGUAGCUUGU	gi 64953 X56316
CAAGCAUUUUGUAGCUUGU	gi 35135 X55362
CAAGCAUUUUAUAGCUUGU	gi 200123 M87223
CAAGCAUUUUGUAGCUUGU	gi 205807 J04791

Figure 76



09310667.051299

KH Release 34 (February 02, 1999) - V.Z.U. - RUVERHIDEN
interleukin-2

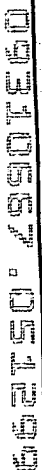
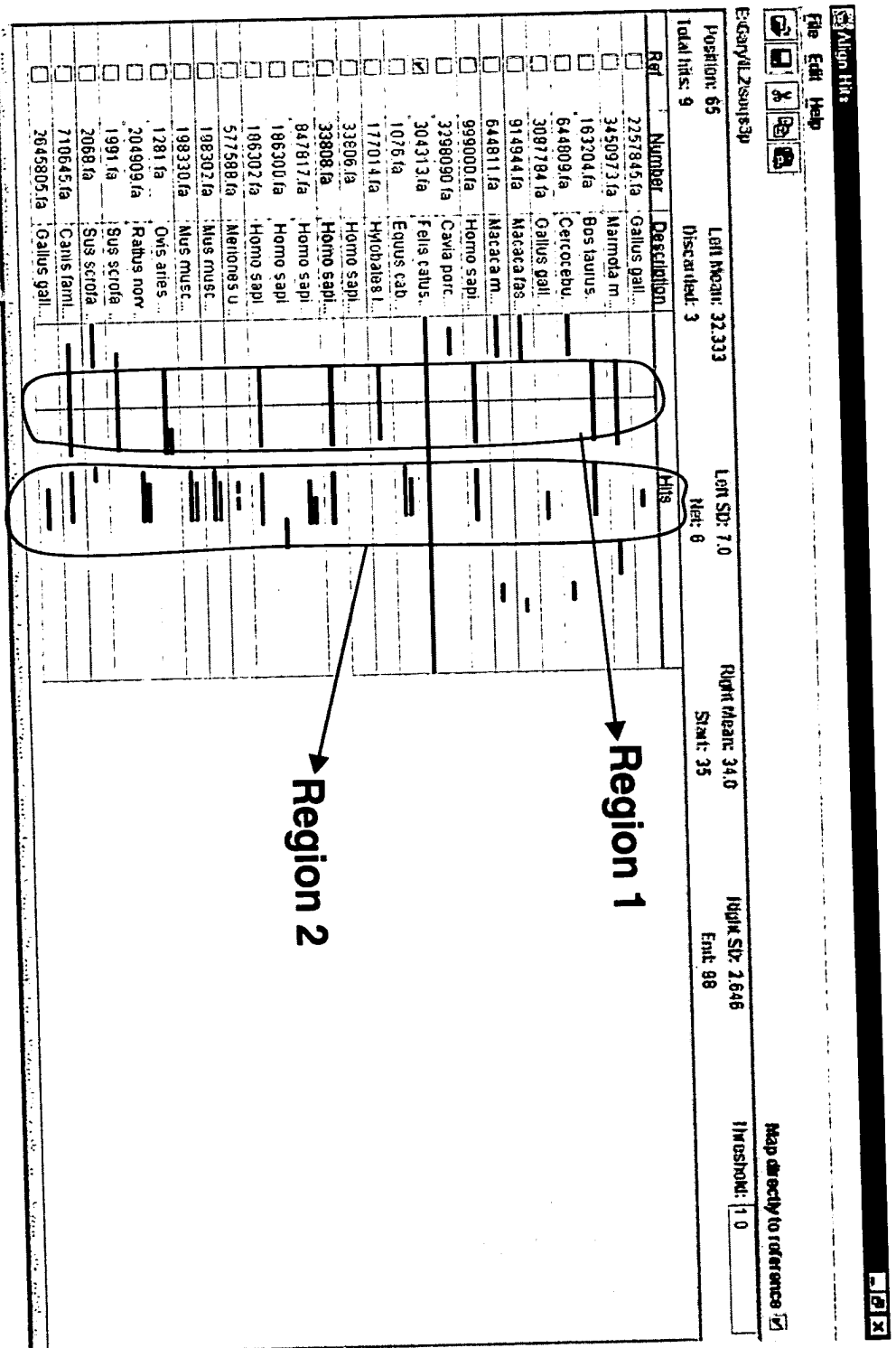


Figure 78



09310667-051299

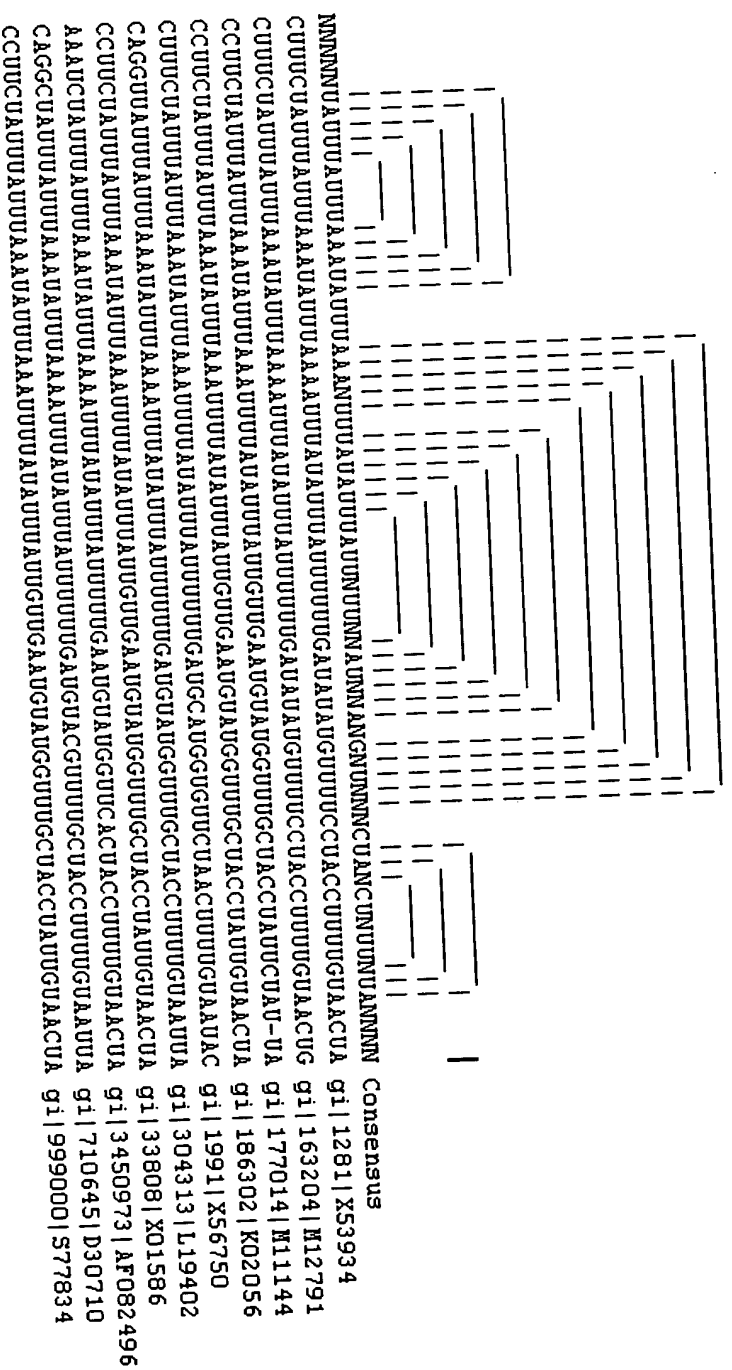
Figure 79

CLUSTAL W (1.74) multiple sequence alignment

```
gi|1281|X53934      CTTCTATTATTAAATATTTAAATTTATATTATTTTGGATATATGTTTTCCTACCTTTGTAACTA
gi|163204|M12791    CTTCTATTATTAAATATTTAAATTTATATTATTATTTTGGATATATGTTTTCCTACCTTTGTAAC TG
gi|177014|M11144    CCTCTATTATTAAATATTTAAATTTTATATTATTATGTTGAATGTAATGCTATGCTACCTAATTCIAI-TA
gi|186302|K02056    CCTCTATTATTAAATATTTAAATTTTATATTATTATGTTGAATGTAATGCTATGCTACCTAATGTAAC TA
gi|1991|X56750      CTTCTATTATTAAATATTTAAATTTTATATTATTATTTTGGATGCAATGCTGCTTAACCTTTGTAATAC
gi|304313|L19402    CAGCTATTATTAAATATTTAAATTTTATATTATTATTTTGGATGTAATGCTATGCTACCTTTTGTAAATTA
gi|33808|X01586     CCTTCTATTATTAAATATTTAAATTTTATATTATTATGTTGAATGTAATGCTACCTAATGTAAC TA
gi|3450973|AF082496 AAATCTATTATTAAATATTTAAATTTTATATTATTATTTTGAATGTAATGCTTCACTACCTTTTGTAACTA
gi|710645|D30710    CAGGCTATTATTAAATATTTAAATTTTATATTATTATTTTGAATGTAACGTTTGTACCTTTTGTAAATTA
gi|999000|S77834    CCTTCTATTATTAAATATTTAAATTTTATATTATTGTTGAATGTAATGCTTGTCTACCTAATGTAAC TA
```

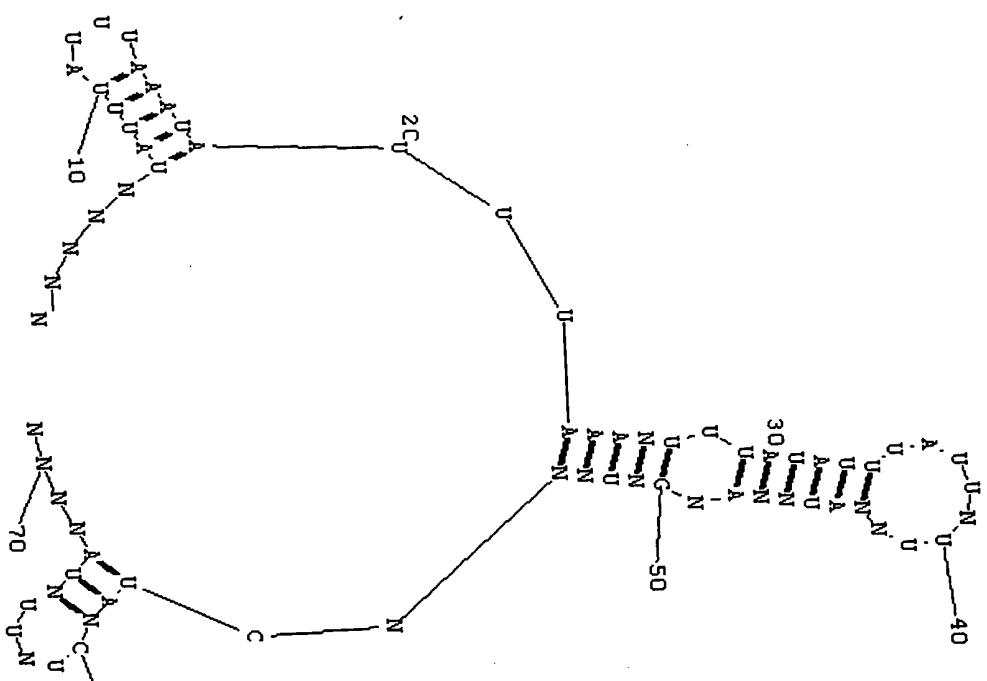
Figure 80

Score: 404.0



09310657 : 051299

Figure 81



09310567.051299

Figure 82

CRYSTAL W (1.74) multiple sequence alignment

g3| 1076|X69393
 g3| 163204|M12791
 g3| 186300|M22005
 g3| 186302|K02056
 g3| 198302|K02797
 g3| 198330|K02292
 g3| 204909|M22899
 g3| 2068|X58428
 g3| 2257845|AF000631
 g3| 2645805|AF033563
 g3| 304313|L19402
 g3| 3087784|AJ224516
 g3| 33808|X01586
 g3| 577588|X68779
 g3| 710645|D30710
 g3| 847817|U25676
 g3| 999000|S77834

031069-05109

Figure 83

Score: 412.0

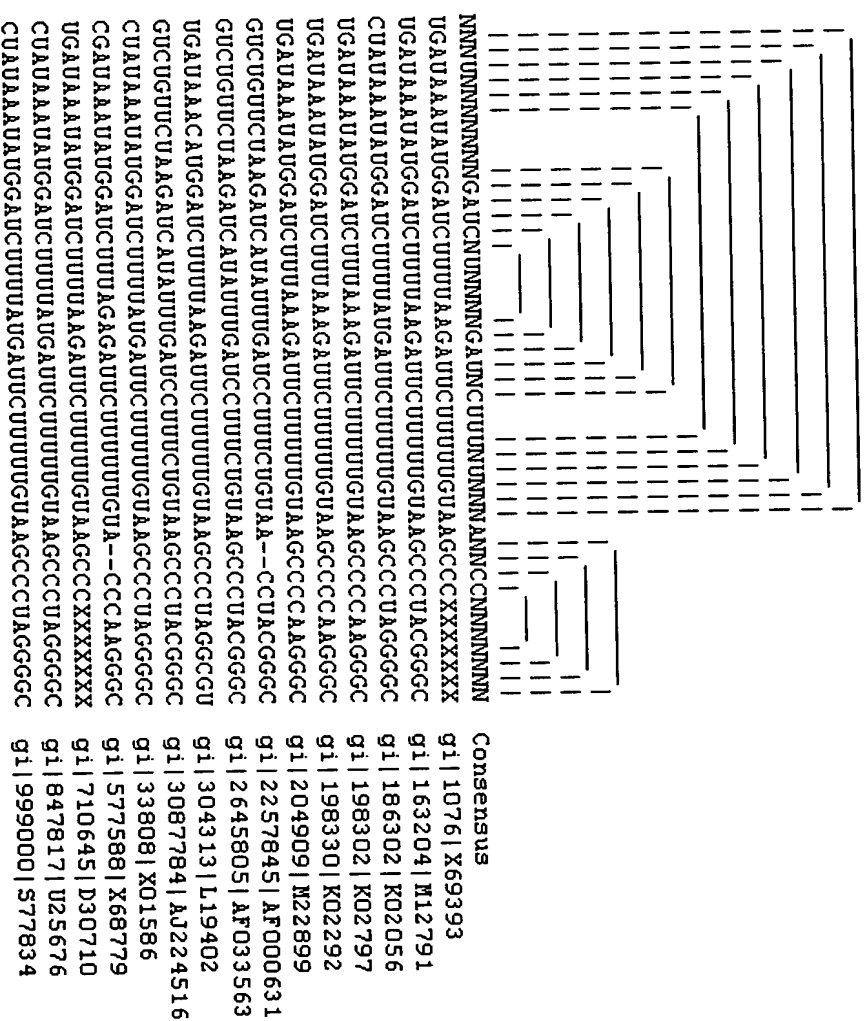


Figure 84

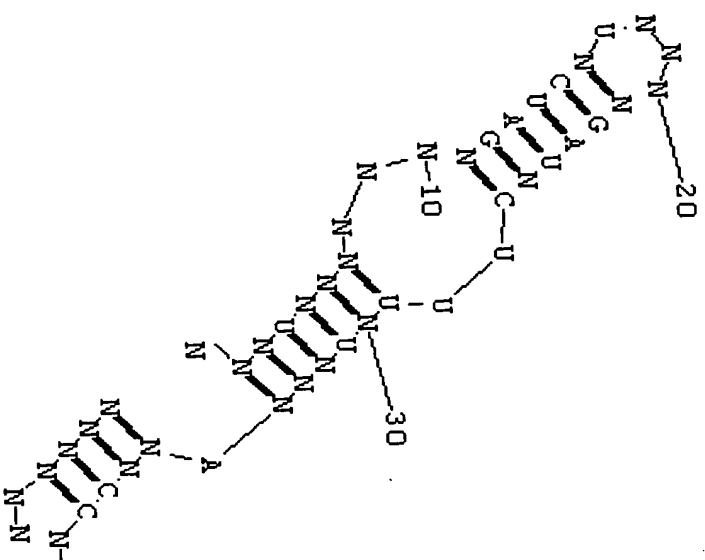


Figure 85

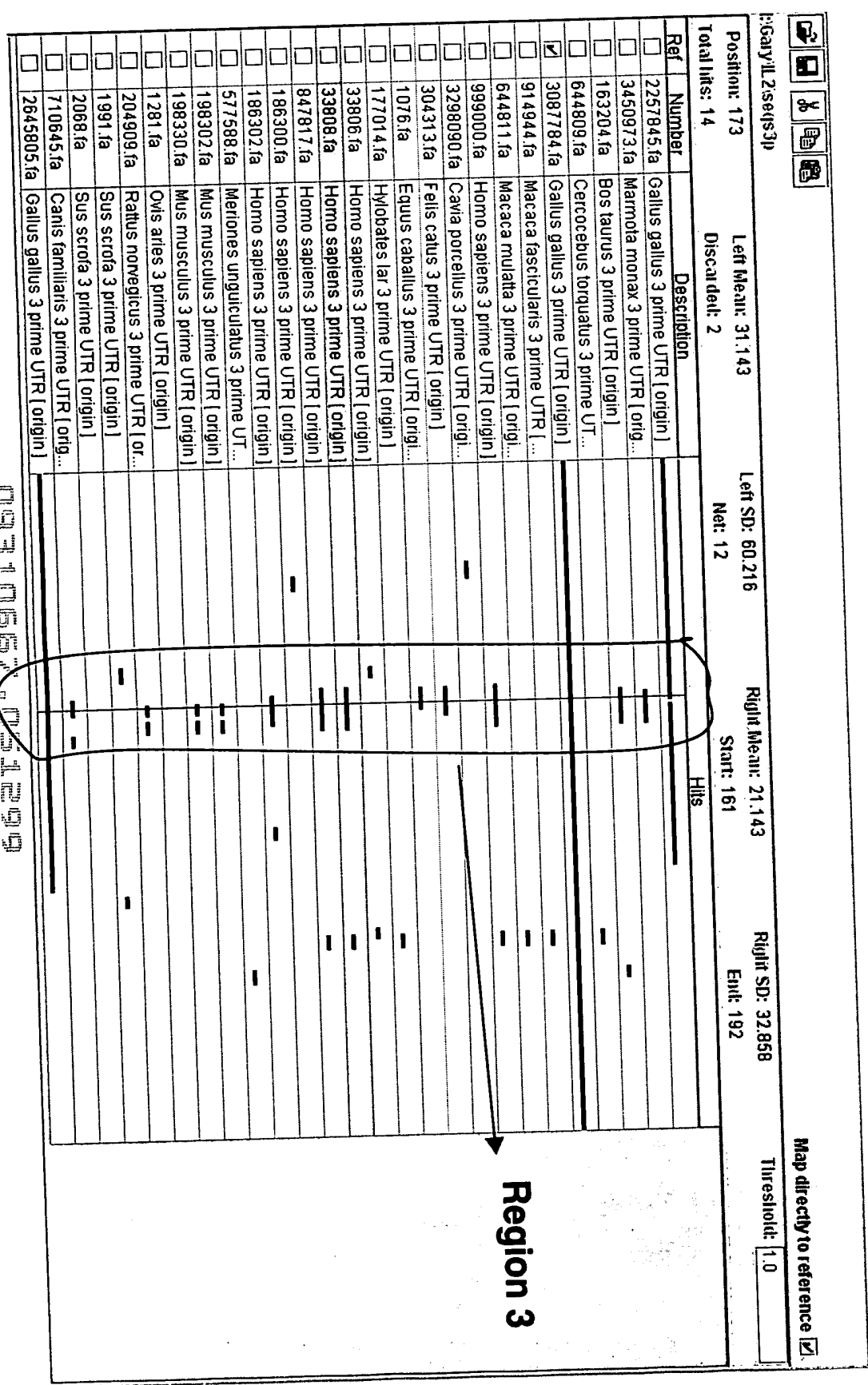


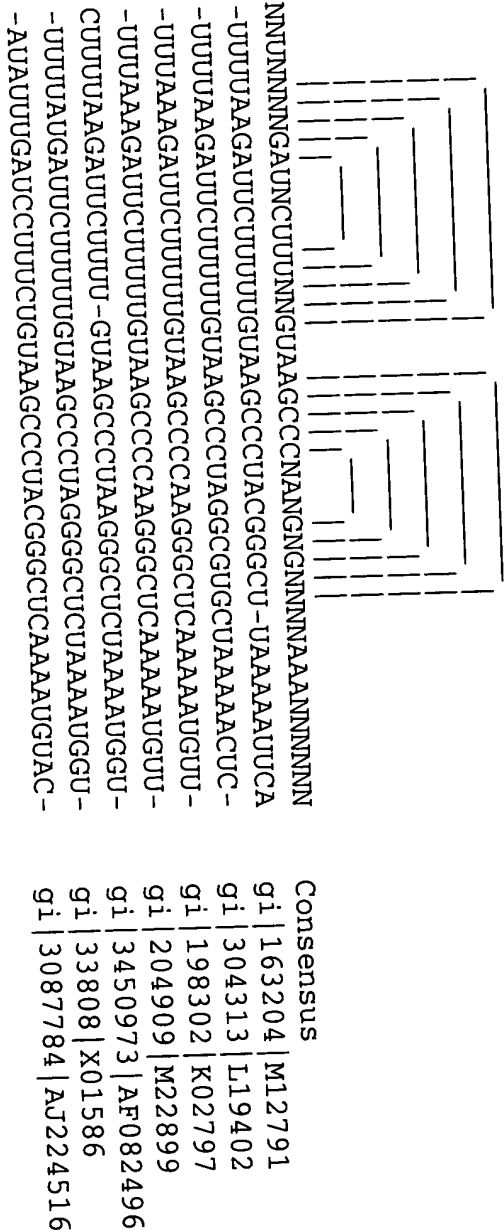
Figure 86

CLUSTAL W (1.74) multiple sequence alignment

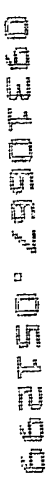
```
gi|163204|M12791      -TTTAAAGATTCTTTTGTAAAGCCCTACGGCT-TAAAAATTCA
gi|304313|L19402      -TTTAAAGATTCTTTTGTAAAGCCCTAGCGTGCTAAAAAACTC-
gi|198302|K02797      -TTTAAAGATTCTTTTGTAAAGCCCCCAAGGCTCAAAAAATGTT-
gi|204909|M22899      -TTTAAAGATTCTTTTGTAAAGCCCCCAAGGCTCAAAAAATGTT-
gi|3450973|AF082496    CTTTAAAGATTCTTTT-GTAAAGCCCTAAGGCTCTPAAAATGGT-
gi|33808|X01586        -TTTATGATTCTTTTGTAAAGCCCTAGGGCTCTAAATGGT-
gi|3087784|AJ224516    -ATATTGATCCTTTCTGTAAAGCCCTACGGGCTCAAAATGTAC-
*      ***      ****      *****      *      *      ***
```

Figure 87

Score: 165.0



2-1



X Release 34 (February 02 1999) - v.2.0 - HOVERGEN
Interleukin 4

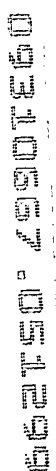
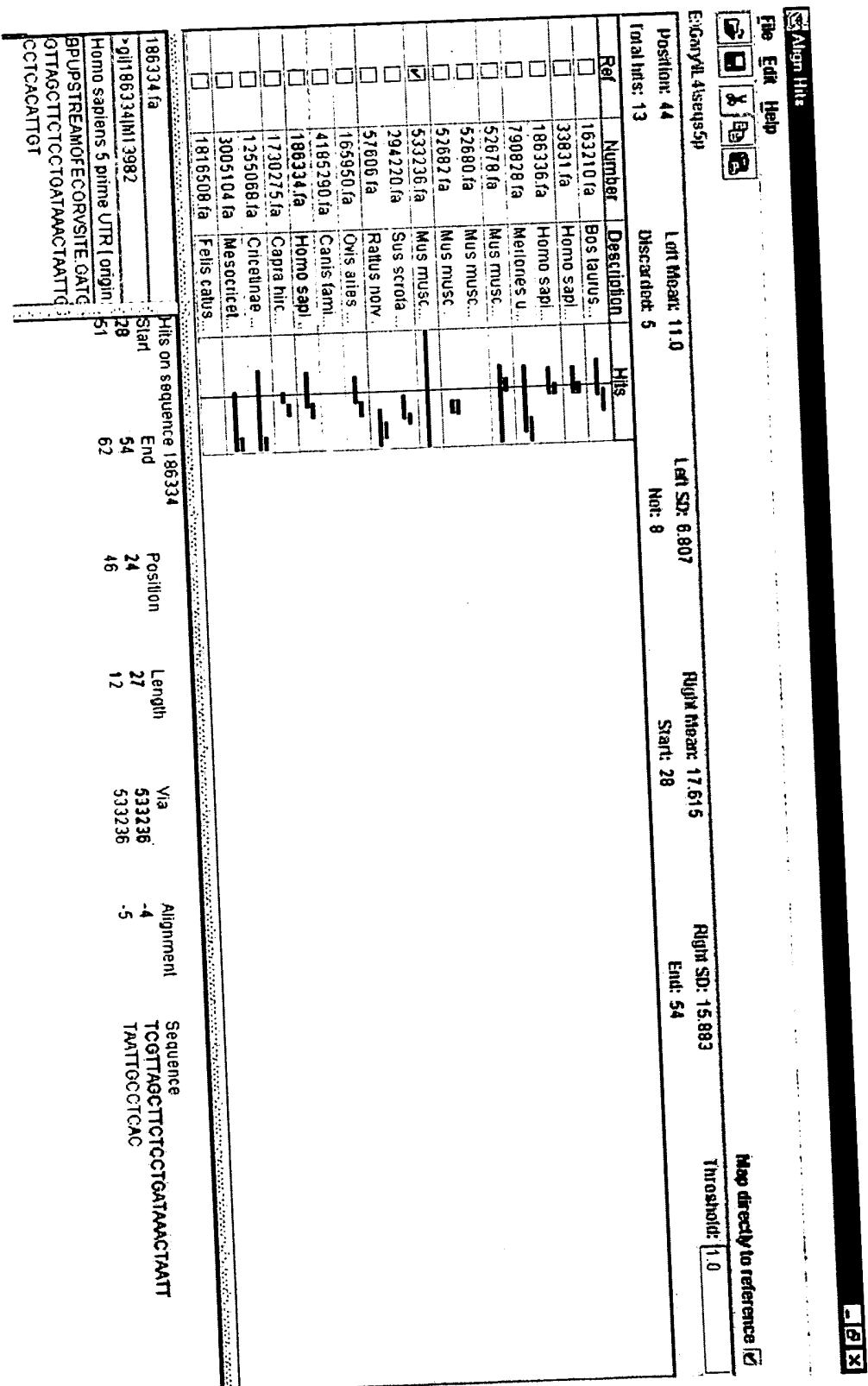


Figure 90



09310667.051299

Figure 91

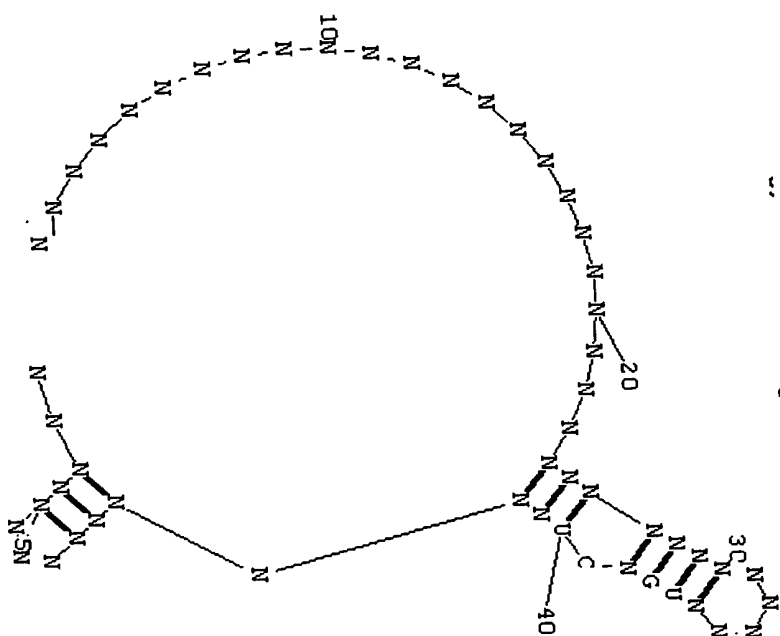
CLUSTAL W (1.74) multiple sequence alignment

```
gi|1255068|U50415      XXXTGCA TTGTTAGCGTCTCTTGATAACCTTAAT-TGTCCTCATCACTGA---
gi|163210|M77120      -XXXXTGCA TTGTTAGCGTCTCTCGTAACTAATTGTCCTCACATTGTCAGT--
gi|165950|M96845      -XXXXXXXXXXXTAGCTTCTCTCGTGAATCTAATTGCCTCACACTGTCAGT--
gi|1730275|U34273      -XXXXXXXXXXXTAGCTTCTCTCGTGAATAACTAATTGCTCTCACACTGTCAGT--
-----GATCGTTAGCTTCTCTCGTGAATAACTAATTGCCCTCACATTGTXXX---
gi|186334|M13982      -GCATTGCATCGTTAGCTTCTCTCGTGAATAACTAATTGCCCTCACATTGTCAGT-
---XXXXXXXXXXXXXXXXXXXXGTAACCTTAATTGCTCTCACATCGTCAGTGC
gi|186336|M23442      XXXXXXXXXXXXXXXXXXXXXXTGATAACCTTAATTGCTCTCACTACTGA---
gi|294220|L12991      -GCATTGCATCGTTAGCTTCTCTCGTGAATAACTAATTGCCCTCACATTGTCAGT-
gi|3005104|AF046213    -GCATTGCATCGTTAGCATCTCTTGATAAACTTAATTGCTCTCGTCACTGA---
gi|33831|X06750      GCATTGCATCGTTAGCATCTCTTGATAAACTTAATTGCTCTCGTCACTGA---
gi|52678|X05064      -GTGTCGCAAGCAGACTTCTTGATA-TTACTCTGTCTTTCCCCAGGGCGA-
gi|52678|X05064b      XXXXXXXXXXXCCAGCCCGACAGCGAGACCCAAATCTGCTCACAAATGAAAC---
gi|52682|X05253      GGGGGGATTGTTAGCATCTCTTGATAAACTTAATTGCTCTCGTCACTGA---
gi|533236|M25892      XXXXXXXAATTGTTGCATCTCTTGACAACTTAATTGCTCTCACATCCCTGA---
gi|790828|L37779
```

[illegible]

Consensus
gi|1255068|U50415
gi|163210|M77120
gi|165950|M96845
gi|1730275|U34273
gi|186334|M13982
gi|186336|M23442
gi|294220|L12991
gi|3005104|AF046213
gi|33831|X06750
gi|52678|X05064
gi|52678|X05064b
gi|52682|X05253
gi|533236|M25892
gi|790828|L37779

Figure 93



09310667.051299

Figure 94

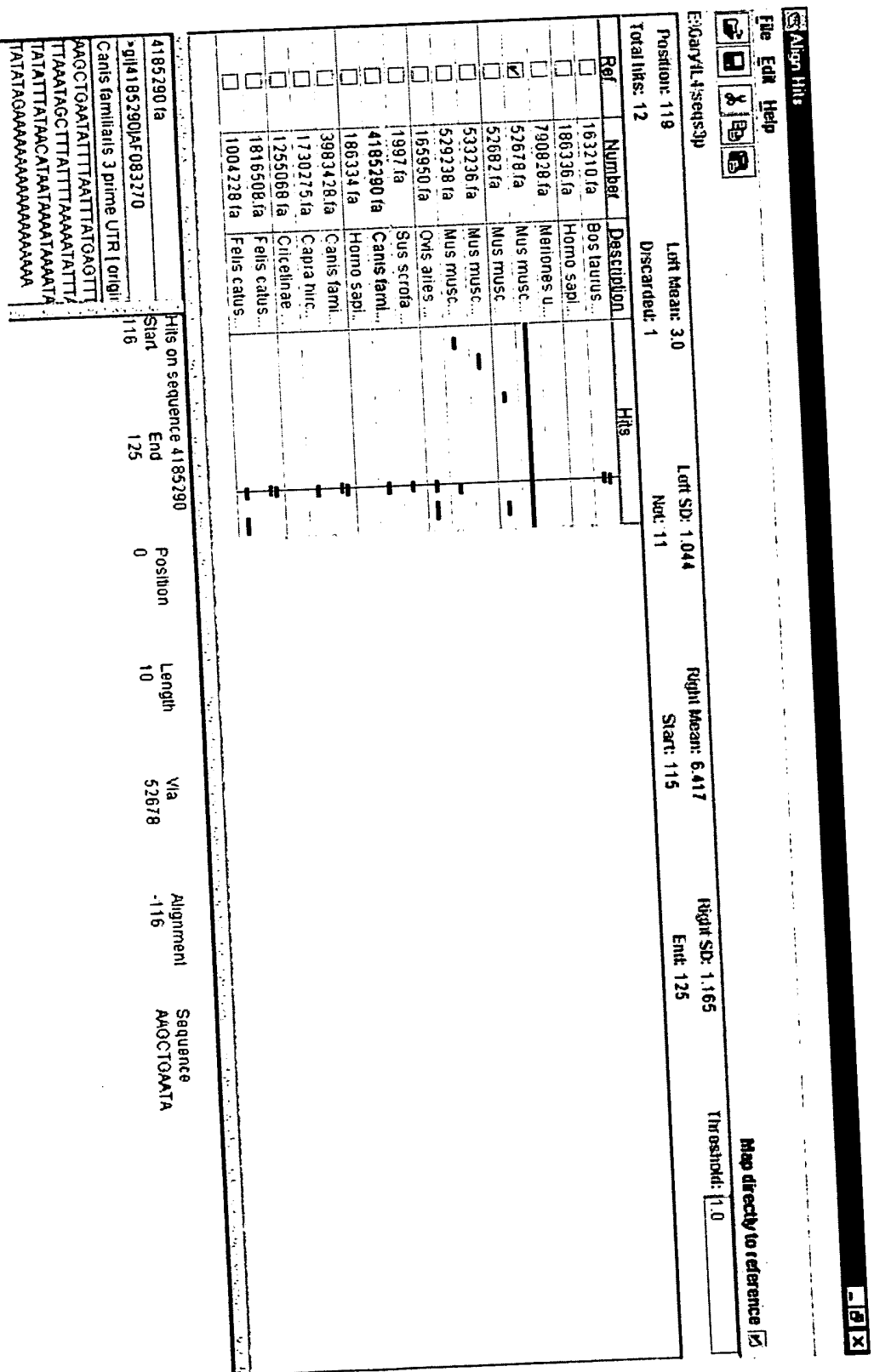


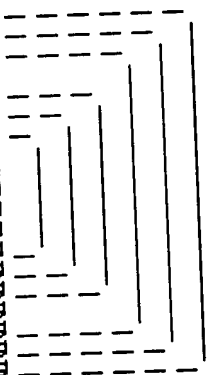
Figure 95

CLUSTAL W (1.74) multiple sequence alignment

```
gi|1004228|X87408      TTATAATTATTATAAATAAGTATATGT-
gi|1004228|X87408b    XXXXXAAGCTGAATATCTTAATTATGAG
gi|163210|M77120      ATGTAGAGCTGAAAAAAXXXXXXXXXXX
gi|163210|M77120b    XXXXXAAGCTGAATATTTAATTATGAG
gi|165950|M96845      AATTATGCTTTTAAATAGCTTATAT---
gi|165950|M96845b    XXXXXAAGCTGAATATTTAATTATGAC
gi|165950|M96845b    XXXXXAAGCTGAATATTTAATTATGAC
gi|1730275|U34273     ATGTAGAACTGAAAAAAXXXXXXXXXAA
gi|1816508|U39634     XXXXXAAGCTGAATATCTTAATTATGAG
gi|1816508|U39634b   XXXXXAAGCTGACTATTTAATTATGAT
gi|19971X68330        ATATAGACCTAAAAAAXXXXXXXXXXX
gi|3983428|AF104245   XXXXXAAGCTGAATATTTAATTATGAG
gi|3983428|AF104245b XXXXXAAGCTGAATATTTAATTATGAG
gi|4185290|AF083270  ACACGAATCTGAATGAAGATGCCGTGAT
gi|52678|X05064       ACTTCATTGCCATAAGGTTCTACTGTTAG
gi|52682|X05253       ATAAAAAACAAACTTCCXXXXXXXXXX
gi|529238|L32955      GTGTCCCACTGAAGGACCAAGGCTCAGGC
gi|529238|L32955b
```

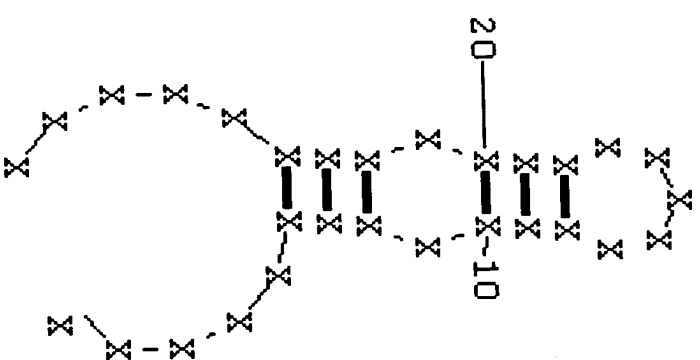
Figure 96

Score: 136.0

[illegible]

0310657 051299

Figure 97



09310657.051299